

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

**Nucleic acids =** organic acids containing nucleic acids.

run on: November 15, 2002, 02:08:58 ; Search time 51 Seconds  
 nucelic search, using sw move1  
 (without ligaments)  
 3589,922 Million cell updates/sec

title: US-09-575-580B-2  
perfect score: 597

scoring table: IDENTITY\_NUC\_GCGC\_100\_Scanout 1 2

searched: 441362 seqs, 153338381 residues

Dear number of this satisfying chosen parameters:

Maximum Match 100%  
Listing first 45 summaries

```
database : Issued_Patents_NA::*  
1: /cgns2.6/Ptodata/1/ina/5
```

2: /etc/init.d/gdm start  
3: gdm

```
4: /cgns-6/ptodata/1/ina/6B_COMB_seq:*
5: /cgns-6/ptodata/1/ina/PCTUS_COMB_seq
6: /cgns-6/ptodata/1/ina/backfiles1
```

Pred. No. is the number of results predicted by chs score greater than or equal to the score of the result.

and is derived by analysis of the total score distribution.

200

result	Query				Score	Match	Length	DB	ID	Description
	No.	Score	Match	Length						
1	398	66.7	2174	2	US-08-665-040-1	Sequence 1, Appli				
2	384	6.4	3303	1	US-08-081-610-3	Sequence 3, Appli				
3	c	6.3	7218	1	US-08-232-463-14	Sequence 14, Appli				
4	c	6.3	7130	4	US-09-105-101-31	Sequence 11, Appli				
5	c	6.2	50937	4	US-09-428-517-1	Sequence 1, Appli				
6	c	6.1	6328	4	US-08-913-832A-1	Sequence 1, Appli				
7	c	6.1	6328	4	US-09-249-178A-1	Sequence 1, Appli				
8	c	6.0	911	2	US-08-759-9	Sequence 9, Appli				
9	c	6.0	911	3	US-09-248-335-9	Sequence 9, Appli				
10	c	5.7	1296	1	US-07-816-283-9	Sequence 9, Appli				
11	c	5.7	1296	1	US-08-417-103-9	Sequence 9, Appli				
12	c	5.7	2118	4	US-09-221-01/B-789	Sequence 789, App				
13	c	5.6	2277	1	US-08-676-967-2	Sequence 2, Appli				
14	c	5.6	2277	1	US-08-676-974-2	Sequence 2, Appli				
15	c	5.6	2277	2	US-09-098-487-2	Sequence 2, Appli				
16	c	5.6	2289	4	US-09-312-038-3	Sequence 3, Appli				
17	c	5.5	2089	1	US-08-557-142A-1	Sequence 1, Appli				
18	c	5.5	2089	1	US-08-910-973-1	Sequence 1, Appli				
19	c	5.5	2089	4	US-09-499-227-1	Sequence 1, Appli				
20	c	5.5	2089	5	PCT/US95-05741-1	Sequence 1, Appli				
21	c	5.5	4221	4	US-09-651-656-22	Sequence 22, Appli				
22	c	5.5	4221	4	US-09-650-855-22	Sequence 22, Appli				
23	c	5.4	602	4	US-09-470-191-81	Sequence 81, Appli				
24	c	5.4	21398	4	US-08-961-527-20	Sequence 20, Appli				
25	c	5.4	435	4	US-09-397-787-282	Sequence 282, App				
26	c	5.4	16432	3	US-08-781-991-208	Sequence 208, App				
27	c	5.3	3489	2	US-08-728-322A-1	Sequence 1, Appli				

ALIGNMENTS

RESULT 1  
US-08-665-040-1  
; Sequence 1, Application US/08665040  
; Patent No. 5869318  
GENERAL INFORMATION:  
; APPLICANT: ESTIVILL PALLEJA, XAVIER  
; APPLICANT: FUENTES, JUAN JOSE  
; APPLICANT: PRITCHARD, MELANIE  
TITLE OF INVENTION: A NEW GENE SEQUENCE OF THE  
DOWN SYNDROME CRITICAL REGION OF HUMAN CHROMOSOME 21.  
; TITLE OF INVENTION: IDENTIFIED BY A NEW "ALU-SPLICING PCR" TECHNIQUE,  
; TITLE OF INVENTION: CODING FOR A PROLINE-RICH PROTEIN (DSCR1) HIGHLY  
; TITLE OF INVENTION: EXPRESSED IN FOETAL BRAIN AND IN HEART AND METHOD  
; TITLE OF INVENTION: FOR CHARACTERIZING IT.

NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LADAS & PARRY  
 STREET: 26 WEST 61ST STREET  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10023  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORD PERFECT 5.1 FOR DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/665,040  
 FILING DATE: JUNE 7, 1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: ES P9501140  
 FILING DATE: JUNE 7, 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JANET I. CORD  
 REGISTRATION NUMBER: 33,778  
 PREFERENCE/DOCKET NUMBER: U010815-9  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 708-1800  
 TELEFAX: (212) 246-8959  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2174 base Pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: circular  
 MOLECULE TYPE: cDNA for mRNA  
 HYPOTHETICAL: No  
 ANTI-SENSE: No

ORIGINAL SOURCE: human  
 ORGANISM: Homo sapiens  
 DEVELOPMENTAL STAGE: foetal  
 TISSUE TYPE: Brain  
 IMMEDIATE SOURCE: gene library of cDNA  
 LIBRARY: gene library of cDNA from foetal  
 CLONE: BC-17.8-1 and BC-17.8-2  
 POSITION IN GENOME:  
 CHROMOSOME SEGMENT: chromosome 21/YAC 72H9  
 MAP POSITION: 21q22.1-q22.2  
 FEATURE:  
 NAME/KEY: cDNA for mRNA, BC-17.8  
 LOCATION: 1...2174  
 FEATURE:  
 NAME/KEY: untranslated 5'  
 LOCATION: 1..48  
 FEATURE:  
 NAME/KEY: coding sequence  
 LOCATION: 49..560  
 OTHER INFORMATION: Down Syndrome critical  
 FEATURE:  
 NAME/KEY: DSCR1  
 LOCATION: 1..171 PEPTIDES  
 IDENTIFICATION METHOD: translation of the  
 OTHER INFORMATION:  
 OTHER INFORMATION: deduced protein domains  
 OTHER INFORMATION: proline-rich protein domains  
 OTHER INFORMATION: glutamic acid-rich protein domains  
 OTHER INFORMATION: leucine/phenylalanine-rich protein domains  
 OTHER INFORMATION:  
 NAME/KEY: untranslated 3'  
 LOCATION:  
 FEATURE:  
 NAME/KEY: 2 Poly (A)  
 LOCATION: 1541..1546 AND 2132..2137  
 US-08-665-040-1

Query Match 66.7%; Score 398; \ DB 2; Length 2174;  
 Best Local Similarity 87.6%; Pred. No. 2.3e-109; Gaps 1;  
 Matches 441; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

Qy 88 GCCAAATTTGAACTCTTCAAGCATATGACAAGAACCAACCCATTCCAGATTAAAG 147  
 Db 58 GCCAATTTGAACTCTTCAAGCATATGACAAGAACCAACCCATTCCAGATTAAAG 117

Qy 148 AGCTTCAAACTGTGGATAAACTTCGCCAACCCCTATGCCAGGATGCCAGGCG 207  
 Db 118 AGCTTCAAACTGTGGATAAACTTCGCCAACCCCTATGCCAGGATGCCAGGCG 177

Qy 208 CGGCTGCACAGACCCGTTCTGGAGGAATGAAAGTGTTATTTGTCAGACTTA 267  
 Db 178 CAGCTGATAAGACTGAGTTCTGGAAANGGAATGAGTTATTTGTCAGCTTA 237

Qy 268 CACATGAAAGTTCACACCTGCTGGCCAAACAGTCATCTCCCT 327  
 Db 238 CACATGAAAGTTCACACCTGCTGGCCAAATCAGAAAGTTCATCTCCCT 297

Qy 328 CGGCCCTCCCTCCGCTGGCCAGAACGTTGAGTGGCCAGGAACTGGCT 387  
 Db 298 CCCGGCTCCGGCAAGGGTGGTGGAAACACTGGAGATCGACCCAGTCATACTAT 357

Qy 388 GATCTTTATATGCCATTCGCTGGCCAGGAGAAGTGAATGACTGCATGCACCG 447  
 Db 358 GATCTTTATATGCCATTCGCTGGCCAGGAGAAGTGAATGACTGCATGCACCG 417

Qy 448 ACAGACCCCACTCCGATCTGGCTGGTGGAGTGGAGACTGGCTGGGCTGGG 507  
 Db 418 ACTGAACTACCTCCAGCTGGTGGCTCATGATGAGTGAATGAGTGAAGGAGA 477

Qy 508 GAGGAGAAGATGGAGAAATGAAGACCAAATCATCCAGACAGGAGA 567  
 Db 478 GAGGAGAAGATGGAGAAATTAAGCCGAACTTAAGCCGAAATGGAGGAGG 534

Qy 568 CCGGAGTAGCACACCGATCCACCTTAAGCTGA 597  
 Db 535 CCGSAGTAGACCGCGATCCACCTTAAGCTGA 564

RESULT 2  
 Sequence 3, Application US/08081610  
 Patent No. 5415941  
 GENERAL INFORMATION:  
 APPLICANT: Yang, Na  
 TITLE OF INVENTION: Materials and Methods for Screening  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Allegretti and Witcoff, Ltd.  
 STREET: 10 S. Wacker Dr.  
 CITY: Chicago  
 STATE: IL  
 COUNTRY: U.S.A  
 ZPP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/081..610  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Heaphy, Barbara A  
 REGISTRATION NUMBER: 34,619  
 REFERENCE/DOCKET NUMBER: 93,402  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-715-1000  
 TELEFAX: 312-715-1234  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3303 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: mRNA  
 LOCATION: 2170..3303  
 FEATURE:  
 NAME/KEY: mRNA  
 LOCATION: 2214..3303  
 FEATURE:  
 NAME/KEY: mRNA  
 LOCATION: 2219..3303  
 FEATURE:  
 NAME/KEY: misc\_RNA  
 LOCATION: 3301..3303  
 OTHER INFORMATION: /note= "CDS Start, codon start = 1,  
 OTHER INFORMATION: /note= "CDS Stop, codon start = 1,  
 OTHER INFORMATION: /note= "translation M"  
 FEATURE:  
 NAME/KEY: TATA-signal  
 LOCATION: 2170..2176  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 1896..2306  
 OTHER INFORMATION: /note= "pB-301  
 -301 to +110"  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 1976..2306  
 OTHER INFORMATION: /note= "pB-221  
 -221 to +110"  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 2106..2306  
 OTHER INFORMATION: /note= "pB-91  
 -91 to +110"



APPLICANT: Tang, Li  
 TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE  
 FILE REFERENCE: 30062-20029.00  
 CURRENT APPLICATION NUMBER: US/09/428,517  
 CURRENT FILING DATE: 1999-10-28  
 EARLIER APPLICATION NUMBER: 60/120,254  
 EARLIER FILING DATE: 1999-02-16  
 EARLIER APPLICATION NUMBER: 60/106,100  
 EARLIER FILING DATE: 1998-10-29  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 1  
 LENGTH: 50937  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE: Description of Artificial Sequence: Recombinant  
 OTHER INFORMATION:  
 JUS-09-428-517-1  
 Query Match 6.2%; Score 37.2; DB 4; Length 5093  
 Best Local Similarity 56.6%; Pred. No. 0, 63; Indels  
 Matches 69; Conservative 0; Mismatches 53; Indels  
 QY 2 TGGAGGAGGTGATCTGAGGACTCCACCATGCCGAGCTGCACCTGGCACTCTGGAA  
 8767 tGAGGGCTGGTGAATCGGGTGGACTCGGGACCGGTGACAGCGACTCGGCCTCCGGCTGC  
 Db 62 GCGCTGTTGAGGGCCTGTCGGGCCAAATTGAAATCCCTCTAGAACAT  
 QY 62 TGGAGGAGGTGATCTGAGGACTCCACCATGCCGAGCTGCACCTGGCACTCTGGAA  
 Db 8827 GCGGCTCTTCGACCCGGGCACTGGACGGCCACCCGAGCC  
 QY 122 AG 123  
 Db 8887 CG 8888  
 RESULT 6  
 US-08-913-832A-1 Application US/08913832A  
 ; Sequence 1, Application US/08913832A  
 ; Patent No. 6339517  
 ; GENERAL INFORMATION:  
 ; APPLICANT: See119; Hans Peter  
 ; APPLICANT: Renz, Manfred  
 ; TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN  
 ; FILE REFERENCE: 84-84-0030-99  
 ; CURRENT APPLICATION NUMBER: US/08/913, 832A  
 ; CURRENT FILING DATE: 1998-01-12  
 ; PRIORITY CLAIMS: PCT/DE96/00444  
 ; PRIORITY FILING DATE: 1996-03-08  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSEQ For Windows Version 4.0  
 ; SEQ ID NO: 1  
 ; LENGTH: 6328  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(5736)  
 US-08-913-832A-1  
 Query Match 6.1%; Score 36.2; DB 4; Length 6  
 Best Local Similarity 53.1%; Pred. No. 0, 5; Mismatches 68; Indels  
 Matches 77; Conservative 0; Mismatches 68; Indels  
 Qy 421 GGAGAAAGTGAATGCACTGGCAGGACAGACCCACTCCAGTGCTGCTGG  
 Db 4921 GTGAGGAAGTGGAAAGTCAGCAATAGATCTGACCCATTGTTGTA  
 Qy 481 TGTGAGATGACCAAGAGATAATGGGAGAAAGGGAGAGATGGGAGAATG  
 Db 4981 GAAGAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAATG  
 Qy 541 AAGCCCCAAATCATCCAGACCGA 565

```

RESULT 7
US-09-249-181A-1 Sequence 1, Application US/09249181A
Db 5041 AAGGACTCTGGATGATGAGAACAGA 50655
; Patent No. 6440679
; GENERAL INFORMATION:
; APPLICANT: Seelig, Hans Peter
; APPLICANT: RENZ, Manfred
; TITLE OF INVENTION: DERMATOMYOSITIS-
; FILE REFERENCE: 8484-A0059-999
; CURRENT APPLICATION NUMBER: US/09/24
; CURRENT FILING DATE: 1998-02-12
; PRIORITY NUMBER: US 08/9113,
; PRIORITY FILING DATE: 1998-01-12
; PRIORITY APPLICATION NUMBER: PCT/DE96/008
; PRIORITY FILING DATE: 1996-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO: 1
; LENGTH: 6328
; TYPE: DNA
; ORGANISM: HOMO sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (5736)
; US-09-249-181A-1

Query Match Score
Best Local Similarity 53.1%; pre-
Matches 77; Conservative 0; M
Matches 77; Conservative 0; M

Qy 421 GGAGAGAACTGATGAACTGATGCAGCGG
| | | | | | | | | | | | | | | | | | | |
Db 4921 GTAGAGAAGTTGGAGAAAGTCACCA

Qy 481 TGTGAGTGTGACCAGAGAATGAGGAG
| | | | | | | | | | | | | | | | | | | |
Db 4931 GAGAGAGAAAGAGAAGAGAGAGAGA

Qy 541 AACCCAAAATCATGCCAGACAGGA 5
| | | | | | | | | | | | | | | | | | | |
Db 5041 AAGGACTCTGGATGAGAACAGA 5

RESULT 8
US-08-924-759-9 Sequence 9, Application US/08924759
; Patent No. 5962229
; GENERAL INFORMATION:
; APPLICANT: MCGRONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: PLANT GLUT
; TITLE OF INVENTION: ENZYME
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE N
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF A
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT
; SOFTWARE: MICROSOFT WORD VE
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/9
; FILING DATE:
; CLASSIFICATION: 435
;
```

ATTORNEY/AGENT INFORMATION:  
 NAME: FLOYD, LINDA AXAMETHY  
 REGISTRATION NUMBER: 33,692  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 302-892-8112  
 TELEFAX: 302-773-0164  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 911 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 TISSUE TYPE: MAIZE  
 IMMEDIATE SOURCE:  
 CLONE: CC71SE-B.PK0014.B8

US-08-924-759-9

Query Match 6.0%; Score 36; DB 2; Length 911;  
 Best Local Similarity 56.9%; Pred. No. 0.24;  
 Matches 66; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 22 GACCTGGCGGCCAACCATGCGCTGCCACCTGGCAAGGGTGTGGACCCGGCTG 81  
 Db 144 GAGCTCCTGTCACCCGTTGCAZAGAAGGTGGCTCTCACGGCGAC 203

Qy 82 TGCCGGGCCAAATTTGAATTCCTCTCAGAACATATGACAAGGACACCCTCCA 137  
 Db 204 GGC GGCCCAUTCTCCAGTCCTCGTCATCCCGACTACCTCGAGGGCTTGA 259

---

RESULT 9  
 US-09-248-335-9  
 Sequence 9, Application US/09248335  
 Patent No. 6096504

GENERAL INFORMATION:  
 APPLICANT: MCGRONIGLE, BRIAN  
 APPLICANT: O'KEEF, DANIEL  
 TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES  
 FILE REFERENCE: CL-1128-A  
 CURRENT APPLICATION NUMBER: US/09/248,335  
 CURRENT FILING DATE: 1999-02-10  
 EARLIER APPLICATION NUMBER: 08/924,759  
 EARLIER FILING DATE: 1997-September-05  
 NUMBER OF SEQ ID NOS: 74  
 SOFTWARE: Microsoft Word Version 7.0A  
 SEQ ID NO 9  
 LENGTH: 911  
 TYPE: DNA  
 ORGANISM: maize

US-09-248-335-9

Query Match 6.0%; Score 36; DB 3; Length 911;  
 Best Local Similarity 56.9%; Pred. No. 0.24;  
 Matches 66; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 22 GACCTGGGCCAACATGGCTGCCACCTGGACCCGGCTGTCGACGGCCTG 81  
 Db 144 GAGCTCCTGTCACCAACCCGTTGCAZAGAAGGTGGCTCTCACGGCGAC 203

Qy 82 TGCCGGGCCAAATTTGAATTCCTCTCAGAACATATGACAAGGACACCCTCCA 137  
 Db 204 GGC GGCCCAUTCTCCAGTCCTCGTCATCCCGACTACCTCGAGGGCTTGA 259

---

RESULT 10  
 US-07-816-283-9  
 Sequence 9, Application US/07816283  
 Patent No. 5436155

GENERAL INFORMATION:  
 APPLICANT: Bell, Graeme I.  
 APPLICANT: Yamada, Yuichiro  
 TITLE OF INVENTION: SOMATOSTATIN RECEPTORS  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77210

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/816,283  
 FILING DATE: 19911231  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNamee, C. Steven  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 713-787-1400  
 TELEX: 79-0924  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1296 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA

US-07-816-283-9

Query Match 5.7%; Score 34; DB 1; Length 1296;  
 Best Local Similarity 56.1%; Pred. No. 1.1;  
 Matches 64; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 469 GTGGTCCACCGTGAGTGAGTGACCAAGAGATGAGGGAGAGATGGGAGAGA 528  
 Db 1051 GTGGGCCCGCGAGAGACTGGGGAGGGATGGGAGAGATGGGAGAGC 1110

Qy 529 ATGAAAGAGACCCAAAGCCAAATCATCCAGACAGGAGACCGAGTACACCCG 582  
 Db 1111 AGGGAGGGCAAGGGAAAGGAGATAACGGCCGGTCAAGCAGTCACCGAG 1164

RESULT 11  
 US-08-417-103-9  
 Sequence 9, Application US/08417103  
 Patent No. 5723299

GENERAL INFORMATION:  
 APPLICANT: Bell, Graeme I.  
 APPLICANT: Yamada, Yuichiro  
 TITLE OF INVENTION: SOMATOSTATIN RECEPTORS  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: United States of America  
 ZIP: 77210

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:





**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### OM nucleic - nucleic search, using sw model

Run on: November 15, 2002, 00:52:13 ; Search time 2653 Seconds  
(without alignments)  
6548.954 Million cell updates/sec

Title: US-09-575-580B-2

Perfect score: 597

Sequence: 1 atggaggaggatggatctgca.....caccatccacccatgtcgta 597

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Result No.	Score	Query			Match			Length	DB ID	Description
		Match	Length	DB	Match	Length	DB			
1	597	100.0	597	10	AF237789	100	mus muscu	597	AX365312	Sequence
2	597	99.2	621	10	AF282255	99.2	Mus muscu	597	AX365312	Sequence
3	592.2	99.2	2125	10	AF260717	99.2	Mus muscu	597	AX365312	Sequence
4	592.2	86.4	597	6	AX365315	86.4	Mus muscu	597	AX365312	Sequence
5	515.8	86.4	597	10	AF237790	86.4	Mus muscu	597	AX365312	Sequence
6	515.8	86.4	2141	10	AF263239	86.4	Mus muscu	597	AX365312	Sequence
7	511	85.6	2198	10	BC013551	85.6	Mus muscu	597	AX365312	Sequence
8	511	85.0	2224	10	AF263240	85.0	Mus muscu	597	AX365312	Sequence
9	507.2	80.7	2212	6	AX365324	80.7	Mus muscu	597	AX365312	Sequence
10	481.8	80.7	2227	9	HSU85266	80.7	Homo sapien	597	AX365312	Sequence
11	481.8	80.7	2289	9	BC002864	80.7	Homo sapien	597	AX365312	Sequence
12	481.8	80.7	2407	9	AK092184	80.7	Homo sapien	597	AX365312	Sequence
13	481.8	80.7	2407	9	AB075973	80.7	Rattus no	597	AX365312	Sequence
14	430.8	72.2	626	10	GU60263	72.2	Cricetulus	597	AX365312	Sequence
15	427.8	71.7	2216	10	GU60263	71.7	Cricetulus	597	AX365312	Sequence
16	426.2	71.4	599	6	AX365311	71.4	Cricetulus	597	AX365312	Sequence
17	403.8	67.6	2331	6	AX365321	67.6	Cricetulus	597	AX365312	Sequence
18	403.8	67.6	2346	9	HSU85267	67.6	Homo sapien	597	AX365312	Sequence
19	401.6	67.3	2284	9	HSU85265	67.3	Homo sapien	597	AX365312	Sequence
20	399.6	66.9	2173	6	AX410694	66.9	Homo sapien	597	AX365312	Sequence
21	399.6	66.9	2173	9	HSU85263	66.9	Homo sapien	597	AX365312	Sequence
22	399.6	66.9	2679	9	AK055845	66.9	Homo sapien	597	AX365312	Sequence
23	398	66.7	2331	6	AX365321	66.7	Homo sapien	597	AX365312	Sequence
24	398	66.7	2346	9	HSU85267	66.7	Homo sapien	597	AX365312	Sequence
25	392.8	65.8	2348	6	AX281651	65.8	Homo sapien	597	AX365312	Sequence
26	335	56.1	562	9	HSU53821	56.1	Homo sapien	597	AX365312	Sequence
27	211	35.3	934	6	AX074351	35.3	Homo sapien	597	AX365312	Sequence
28	211	35.3	3159	6	AX420425	35.3	Homo sapien	597	AX365312	Sequence
29	211	35.3	3261	9	AK09090	35.3	Homo sapien	597	AX365312	Sequence
30	207.8	34.8	3240	9	AY034085	34.8	Homo sapien	597	AX365312	Sequence
31	207.8	34.8	3253	9	AY034086	34.8	Homo sapien	597	AX365312	Sequence
32	195.6	32.8	3295	10	AB061525	195.6	Mus muscu	597	AX365312	Sequence
33	193	32.3	3184	6	AX329596	193	Mus muscu	597	AX365312	Sequence
34	193	32.3	3184	6	AX333015	193	Mus muscu	597	AX365312	Sequence
35	193	32.3	3184	6	AX365327	193	Mus muscu	597	AX365312	Sequence
36	193	32.3	3184	6	AX420436	193	Mus muscu	597	AX365312	Sequence
37	193	32.3	3184	9	HUMZAK14	193	Mus muscu	597	AX365312	Sequence
38	186.4	31.2	720	6	AX365333	186.4	Mus muscu	597	AX365312	Sequence
39	186.4	31.2	720	9	AF176117	186.4	Mus muscu	597	AX365312	Sequence
40	186.4	31.2	828	6	AX365330	186.4	Mus muscu	597	AX365312	Sequence
41	186.4	31.2	828	6	AX420437	186.4	Mus muscu	597	AX365312	Sequence
42	186.4	31.2	828	9	AF176116	186.4	Mus muscu	597	AX365312	Sequence
43	184.6	30.9	615	6	AX420432	184.6	Mus muscu	597	AX365312	Sequence
44	183.2	30.7	776	10	AF237888	183.2	Mus muscu	597	AX365312	Sequence
45	183	30.7	594	6	AX365318	183	Mus muscu	597	AX365312	Sequence

#### ALIGNMENTS

RESULT 1	AX365312	597 bp	DNA	PAT 15-FEB-2002
LOCUS	Sequence 2 from Patent WO0204491			
DEFINITION				
ACCESSION	AX365312			
VERSION	AX365312.1			
KEYWORDS				
SOURCE	house mouse.			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus .			
REFERENCE	1			
AUTHORS	Williams,S.R. and Rothermel,B.			
TITLE	Methods and compositions relating to muscle selective calcineurin interacting protein (mcip)			

Pred. No. is the number of results predicted by chance to have a

Fri Nov 15 07:56:43 2002

JOURNAL	Patent: WO 0204491-A 2 17-JAN-2002; Title: Texas System (US) ; Williams, Board of Regents, The University of Texas ; Beverly (US)	
FEATURES	SOURCE	
Sanders R. (US); Rothenberg, Beverly (US)	Location/Qualifiers	
1..597 /organism="Mus musculus" /db_xref="taxon:110090" 1..597 /note="unnamed protein product" /codon_start=1 /protein_id="CAD23808_1" /db_xref="GI:18617044" /translation="MEVEYDQDLSATIAGHLDPRFVYDGLCRAKFESLFRTYDKDTT /translation="MEVEYDQDLSATIAGHLDPRFVYDGLCRAKFESLFRTYDKDTT /PQYFSKPKRVPINFSNPLSAADRLRHKTEFLGKEMILYFACTLHIGSSHAPPND KOFLLSPASPPVGWQKQVEDNAPVINDYLPAISLGPGKEYELHAAATDPTPSVWVHV CESDONNEEEEMERMRKPKKIIQCCRPPYTPHS"	CDS	
160 a 170 c 151 g 116 t		BASE COUNT

ORIGIN		Score	DB	Length	;
Query	Match	100.0%	Score 597;	DB 6;	Length 597;
Best Local Matches	Similarity	100.0%	Pred. No. 1-1e-148;		
Mismatches	Conservative	0;	Mismatches -0;	indels	0;
Qy			Gaps		
Db	1	ATGGAGGAGGGATCCTGGAGGACCTGCAGCACCATTGCCTGCCACCTGGACCG	60		
Qy	1	ATGGAGGAGGGATCCTGGAGGACCTGCAGCACCATTGCCTGCCACCTGGACCG	60		
Db	61	CGGCTGTTGCGTGGACCGCCGTGTCGGGSCCAATTGAATCCCTTCAAGAACATA	120		
Qy	61	CGGCTGTTGCGTGGACCGCCGTGTCGGGSCCAATTGAATCCCTTCAAGAACATA	120		
Db	61	CGCTGTTGCGTGGACGCCCTGTGCCGGAAATTGTAAACTTCAGAACATAGAC	180		
Qy	121	AAGGACACCCPTCAGCTATTTAGAGGTTCAACGTGTCGGATAAACCTTCAGCAC	180		
Db	121	AAGGACACCCPTCAGCTATTTAGAGGTTCAACGTGTCGGATAAACCTTCAGCAC	180		
Qy	181	CCCTATATCTGGAGGGATGCCAGGTGGCTGCCAGGTGGCTGGAGAA	240		
Db	181	CCCTATCTGGAGGGATGCCAGGTGGCTGGAGAAAGCAGGTCTGGAGAA	240		
Qy	241	ATGAAGTGTAAATTGGCTCAAGCTTATCACATAGGAACTTGCTGCAAACTA	300		
Db	241	ATGAAGTGTAAATTGGCTCAAGCTTATCACATAGGAACTTGCTGCAAACTA	300		
Qy	301	CCCCAAACAGCTTCCATCTCCCTGGGCTCTCCCTGGTTGGCTGAACTA	360		
Db	301	CCCCAAACAGCTTCCATCTCCCTGGGCTCTCCCTGGGCTGAACTA	360		
Qy	361	GAAGATGCCACCCCGCATATAATTAGCACTTTATAGCATTCTCAAGTGGCCA	420		
Db	361	GAAGATGCCACCCCGCATATAATTAGCACTTTATAGCATTCTCAAGTGGCCA	420		
Qy	421	GGAGAGAAGTGAATGACTGATGAGGAGAGGAGAGGAGAGGAGAGGAG	480		
Db	421	GGAGAGAAGTGAATGACTGATGAGGAGAGGAGAGGAGAGGAGAGGAG	480		
Qy	481	TGTGAGACTGACCAAGAGAATGAGGAGAGGAGAGGAGAGGAGAGGAG	540		
Db	481	TGTGAGACTGACCAAGAGAATGAGGAGAGGAGAGGAGAGGAGAGGAG	540		
Qy	541	ANGCCCAAATCATCCAGACAGGGACCGGACTACACCCGATACACCTTATGCTGA	597		
Db	541	ANGCCCAAATCATCCAGACAGGGACCGGACTACACCCGATACACCTTATGCTGA	597		
Qy	541	ANGCCCAAATCATCCAGACAGGGACCGGACTACACCCGATACACCTTATGCTGA	597		
Db	541	ANGCCCAAATCATCCAGACAGGGACCGGACTACACCCGATACACCTTATGCTGA	597		

Db	481	TGTGAGTGTACCAAGAATCAGGAAAGAGATGGAGAACCC	540	Qy	181	CCCTTATCTGCAGCCGATGCCAGGTCTGGCTCACAAAGCCGAGTCCTGGGAAGAA	240
Qy	541	AAGGCCAAATCATCCAGACCGGAGAACCGGACTACCCATTAGCTGA	597	Db	188	CCCTTATCTGCAGCCGATGCCAGGTCTGGCTCACAGACCGAGTCCTGGGAAGAA	247
Db	541	AAGGCCAAATCATCCAGACCGGAGAACCGGACTACCCATTAGCTGA	597	Qy	241	ATGAAAGTTGTTATTTGCTCAGACTTACACATAGGAAGTCACACCMGGCTCGCCCAAT	300
RESULT 3				Db	248	ATGAAAGTTGTTATTTGCTCAGACTTACACATAGGAAGTCACCTGGCTCGCCCAAT	307
LOCUS	AF282255	621 bp mRNA linear ROD 11-NOV-2000		Qy	301	CCGGACAAACAGTCCTCATCCCTCCGCTCTCCCGTTGCTGGAAACAGTA	360
DEFINITION	Mus musculus	Down syndrome candidate region 1 protein (Dscr1) mRNA, complete cds.		Db	308	CCGGACAAACAGTCCTCATCCCTCCGCTCTCCCGTTGCTGGAAACAGTA	367
ACCESSION	AF282255			Qy	361	GAGATGCCACCCCGTCATAATTAGCTCATCTCAAGTGGCCA	420
VERSION	AF282255.1	GI:9652249		Db	368	GAGATGCCACCCCGTCATAATTAGCTCATCTCAAGTGGCCA	427
KEYWORD	Mus musculus			Qy	421	GGAGAGAATGTCATGCCGGACAGACCCACTCCAGTGGTGTGGTCACAGTG	480
ORGANISM	Mus musculus			Db	428	GGAGAGAATGTCATGCCGGACAGACCCACTCCAGTGGTGTGGTCACAGTG	487
REFERENCE	Eukyooya; Merazona; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. (bases 1 to 621)			Qy	481	TGNGAGTGTACCAAGAATGGAGAACAGATGGAGAACGAGACGGACGCC	540
AUTHORS	Strippoli,P., Petrini,M., Lenzi,L., Carinci,P. and Zannotti,M.			Db	488	TGNGAGTGTACCAAGAATGGAGAACAGATGGAGAACGAGACGCC	547
TITLE	The murine DSCR1-like (Down syndrome candidate region 1) gene family: conserved synteny with the human orthologous genes			Qy	541	AAGCCCAAATCATCCAGACAGGAGTACACCGGACTACACCCATCCAGTGGCTGA	597
JOURNAL	Gene 257 (2), 223-232 (2000)			Db	548	AAGCCCAAATCATCCAGACAGGAGTACACCGGACTACACCCATCCAGTGGCTGA	604
PUBLISHER	2 (bases 1 to 621)			RESULT 4			
AUTHORS	Strippoli,P., Petrini,M., Lenzi,L., Carinci,P. and Zannotti,M.			AF260717	2125 bp mRNA linear ROD 22-MAR-2001		
TITLE	Direct Submission			DEFINITION	Mus musculus Down syndrome candidate region 1 (Dscr1) mRNA, complete cds.		
JOURNAL	Submitted (24-JUN-2000) Istituto di Istologia ed Embriologia Generale, Università di Bologna, Via Belmeloro, 8, Bologna, BO 40126, Italy			ACCESSION	AF260717		
FEATURES	Location/Qualifiers			VERSION	AF260717.1	GI:7839596	
source	1..621			KEYWORDS			
	/organism="Mus musculus"			ORGANISM	Mus musculus		
	/strain="BALB/C"			REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
CDS	/db_xref="txon:10090"			AUTHORS	1 (bases 1 to 2125)		
	/chromosome="16"			TITLE	Casas,C., Martinez,S., Pritchard,M.A., Fuentes,J.J., Nadal,M., Gimera,J., Arbones,E., Soriano,E., Estivill,X. and Alcantara,S.		
	/sex="male"			DESCRIPTION	Dscr1, novel endogenous inhibitor of calcineurin signaling, is expressed in the primitive ventricle of the heart and during neurogenesis		
	/tissue_type="brain"			JOURNAL	Mech. Dev. 101 (1-2), 289-292 (2001)		
	1..621			MEDLINE	2115220		
gene	/gene="Dscr1"			PUBMED	11231093		
	8..604			REFERENCE	3 (bases 1 to 2125)		
	/gene="Dscr1"			AUTHORS	Fuentes,J.J., Pritchard,M., Puchores,C. and Estivill,X.		
	/note="similar to the Homo sapiens Down syndrome candidate region 1 protein"			TITLE	Down syndrome candidate region 1 (Dscr1), one of three Down syndrome alternatively spliced exon 1		
	/codon_start=1			JOURNAL	unpublished		
	/product="Down syndrome candidate region 1 protein"			MEDLINE	2115220		
	/protein_id="AAF91461_1"			PUBMED	11231093		
	/db_xref="GI:9652250"			REFERENCE	2 (bases 1 to 2125)		
	/product="MEVDIOLPSATIACHILDPRFYDGFICRAFEFLPFYDDDTTFOYFSFKRVRINFNSNPLSAADARLHRHTEFLGKMLFQAOTLHIGSSHLAPRNDCESDQENEEEEMEMKRPKPILTRPPTPLHS"			AUTHORS	Fuentes,J.J., Pritchard,M., Puchores,C. and Estivill,X.		
BASE COUNT	166	a 179 c 159 g 117 t		TITLE	Direct Submission		
ORIGIN				JOURNAL	Submitted (26-APR-2000) Centre de Genetica Medica i Molecular, IRO, Avia. Castelldefels Km. 2,7, L' Hospital de Llobregat, Barcelona 08907, Spain		
				FEATURES	Location/Qualifiers		
Query Match	99.2%	Score 592.2; DB 10; Length 621;		source	1..2125		
Best Local Similarity	99.5%	Pred. No. 2..2e-147;			/organism="Mus musculus"		
Matches	594;	Conservative 0; Mismatches 3; Indels 0; Gaps 0;			/db_xref="taxon:10090"		
Qy	1	ATGGAGGAGGATCTGCAGAACCTGCCAGGCCACATGCCCTGGACCGG 60			/chromosome="16"		
Db	8	ATGGAGGAGGATCTGCAGAACCTGCCAGGCCACATGCCCTGGACCGG 67			1..2125		
Qy	61	CGCGTGTCTGGAGCCGCAAAATTGGAATTCTCTTCAGAACATATGAC 120			/gene="Dscr1"		
Db	68	CGCGTGTCTGGAGCCGCAAAATTGGAATTCTCTTCAGAACATATGAC 127			15..61		
Qy	121	AAGGACACCAACCTCCAGTATTAAAGAGCTCAACAGTGTCCGATAAACCTCAGAAC 180			/gene="Dscr1"		
Db	128	AAGGACACCAACCTCCAGTATTAAAGAGCTCAACAGTGTCCGATAAACCTCAGAAC 187			/note="calcineurin inhibitor"		





KOFLISPPASPPVNGWKOVEDATPVINYDLYAISKLGPEKEYELHAATDTTPSVVVFH  
CESDEEEEMERMRPKPLIQTTRPTEPIHLS"

---

	BASE COUNT	ORIGIN
Qy	533 a	539 c
Qy	557 t	559 g
Query Match	85.6%	Score 511; DB 10;
Best Local Similarity	93.8%	Length 2198;
Matches	532;	Pred. No. 1-2e-125;
Conservative	0;	Mismatches 0;
Indels	35;	Gaps 0;
Qy	31 AGCGCACCATCGCTGCCACCTGCGCCTGGTGGCGCCGTGCGCCGC 90	
Db	107 AGCTCCCTGATTCGTTGCTGGCAAAACGATGATGCTTCAGCGAAAGTGACCGCC 166	
Qy	91 AAATTGAAATCCCTCTCAGAACATGACAAGAACACCCCTTCAGATTAAAGACC 150	
Db	167 AAATTGAAATCCCTCTCAGAACATGACAAGAACACCCCTTCAGATTAAAGACC 226	
Qy	151 TTCAAACTGTTCCGSATAACTTCAGAACGGACCAAGCCAAATCATCCAGAACGGACCG 600	
Db	227 TTCAAACTGTTCCGSATAACTTCAGAACGGACCAAGCCAAATCATCCAGAACGGACCG 286	
Qy	211 CTGCAAAAGCCGACTCTGGGAGGAAATGAGTTGATCAGACTTACAC 270	
Db	287 CTGCAAAAGCCGACTCTGGGAGGAAATGAGTTGATCAGACTTACAC 346	
Qy	271 ATAGAAAGTTCACACCTGCTCCGCACAAAGATTCCTCATCTCCCTCCG 330	
Db	347 ATAGAAAGTTCACACCTGGCTCCGCACAAAGATTCCTCATCTCCCTCCG 406	
Qy	331 GGCCTCCCTCCCGTGGCTCCGGAGGAAATGAGTTGATCAGACTTACAC 390	
Db	407 GGCCTCCCTCCCGTGGCTCCGGAGGAAATGAGTTGATCAGACTTACAC 466	
Qy	391 CTTTATATGCCATCCAGCTGGCTGGCAGAGAACAGTAGAACATGAGCCACCGC 450	
Db	467 CTTTATATGCCATCCAGCTGGCTGGCAGAGAACAGTAGAACATGAGCCACCGC 526	
Qy	451 GACCCCACTCCCASTGTTGTCACGTTGAGTGGACAGAAGATGAGGAA 510	
Db	527 GACACACTCCAGTGGCTGGCAGAGAACAGTAGAACATGAGCCACCGC 586	
Qy	511 GAGGAAGATGGAGAAGTAAGAACGACCCAAGCCAAATCATCCAGACCGACCG 570	
Db	587 GAGGAAGATGGAGAAGTAAGAACGACCCAAGCCAAATCATCCAGACCGACCG 646	
Qy	571 GAGTAACACCGATCACCTTAGCTGA 597	
Db	647 GAGTAACACCCATCACCTCAGCTGA 673	
RESULT	9	
LOCUS	AF263240	
DEFINITION	Mus musculus, Down syndrome critical region homolog 1 (human), clone MGC:19348 IMAGE:4236038, mRNA, complete cds.	
ACCESSION	BC013551	
VERSION	BC013551.1	
KEYWORDS	GI:15488840	
SOURCE	house mouse,	
ORGANISM	Mus musculus	
REFERENCE	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus, 1 (bases 1 to 2188)	
AUTHORS	Straussberg, R.	
TITLE	Direct Submission	
JOURNAL	Submitted (04-SEP-2001), National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK	NIH-MGC Project URL: http://mgc.ncbi.nih.gov	
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov	
Tissue Procurement	Jeffrey E. Green, M.D.	
CDNA Library Preparation	Life Technologies, Inc.	
Gene Collection	National Cancer Institute, Bethesda, MD 20892-2590, USA	
Arranged by	The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing	Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305	
Web site	http://www.shg.c.stanford.edu	
Contact	(Dickson, Mark) med@paxil.stanford.edu	
Dickson, M., Schmutz, J., Rodriguez, A., and Myers, R. M.		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINN, at: <a href="http://Image.linn.gov">http://Image.linn.gov</a>		
Series	IRAK Plate: 25 Row: m Column: 6.	
Location/Qualifiers	1..2198	
FEATURES	source	
CDS	/organism="Mus musculus" /db_xref="taxon:10900" /map="FVB/N" /clone="MGC:19348 IMAGE:4236038" /tissue_type="Kidney, normal, 5 month old male mouse." /clone_id="NCL_CGAP_Kid14" /lab_host="DHIOB" /note="Vector: pCMV-SPORT6" /codon_start=1 /product="Down syndrome critical region homolog 1 (human)" /protein_id="AAH13511" /db_xref="GI:15488841" /db_xref="LocusID:34720" /translation="MHEFRFSYNSLIAVCANDDVSESETRAKEESLERTYDKDTT FQIFSKFKRVRINFSNPLSAA达尔罕人族KEMKLYFAQLHIGSSHAPPNPD	





CDS	66 . 659	/codon_start=1 /product="Down syndrome critical region gene 1" /protein_id="AAH02864_1" /db_xref="GI:12804023" /translation="MEEDLQDLSATIACHLDPRVFDGLCRAKFESLFRYDKDT FYQFYSFKRVRINFSPFSAADRLQLHKTEFLGKMLFAQTQHIGSSHLPNPD KOFLSPPASPVGNKOVEDATPVINYDLYAISKLGPKEYLHAATDTPSPVVHV CESDQEKEEEMMRPMPKIQTRPEYPTIHL"	BASE COUNT ORIGIN	628 a 465 c 555 g 641 t	Query Match Best Local Similarity 89.1%; Score 481.8; DB 9; Length 2289; Matches 532; Conservative 0; Mismatches 66; Indels 3; Gaps 1;	SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL AUTHORS TITLE JOURNAL SUBMISSION DIRECT SUBMISSION COMMENT CONSTRUCTION FEATURES SOURCE ORGANISM="Homo sapiens" /db_xref="taxon:9606" /clone_id="NT2NE2 clone:NT2NE2014104".	Homo sapiens teratocarcinoma cell-line:NT2 CDNA to mRNA, clone:NT2NE2 clone:NT2NE2014104 .	
Qy	1	ATGGAGGAGTGGATCTGAGGACCTCGGCCAGCCATGCCGACGCC 60	Qy	61	CGCGTGTTCGAGGGCCATTGAAATTGAACTCCCTCTAGAACATATGAC 120	Qy	61	CCCTTATCTGGCAGCATGGCTCAGCTGATAGACTGAGTTCTGAG 305
Db	66	ATGGAGGAGTGGATCTGAGGACCTCGGCCAGCCATGCCGACGCC 125	Db	126	CCGGTGTTCGAGGGCCATTGAAATTGAGTCCTCTAGAACATATGAC 185	Qy	121	AGGACACACACTTCCAGTATTAAAGCTCAAAGTGTGGATAAACUTCGAAC 180
Qy	121	AAGGACATCACCTTTCAGTATTAAAGCTCAAAGTGTGGATAAACUTCGAAC 245	Db	186	AAGGACATCACCTTTCAGTATTAAAGCTCAAAGTGTGGATAAACUTCGAAC 245	Qy	181	CCCTTATCTGGCAGCATGGCTCAGCTGATAGACTGAGTTCTGAG 300
Qy	181	CCCTTATCTGGCAGCATGGCTCAGCTGATAGACTGAGTTCTGAG 305	Db	246	ATGAAGTTGTAATTGCTCAGACTTACACATAGGAAGTTCACACCTGGCTCGGCCAAAT 365	Qy	241	ATGAAGTTGTAATTGCTCAGACTTACACATAGGAAGTTCACACCTGGCTCGGCCAAAT 360
Db	306	ATGAAGTTGTAATTGCTCAGACTTACACATAGGAAGTTCACACCTGGCTCGGCCAAAT 365	Qy	301	CCGACAAACAGCTCTCATCTCCCTCCGGCTCTCCGGTGGCTGAAACAGTA 360	Db	366	CCGACAAACAGCTCTCATCTCCCTCCGGCTCTCCGGTGGCTGAAACAGTA 425
Qy	361	GAAGATGCCACCCGTCATAAATTAGATCCTTTATAGCTCAAGCTGGGCCA 420	Qy	361	GAAGATGCCACCCGTCATAAACTATGATCCTCTATATGCCATCICAAGCTGGGCCA 485	Db	426	GAAGATGCCACCCGTCATAAACTATGATCCTCTATATGCCATCICAAGCTGGGCCA 485
Qy	421	GGAGAGAAGTATGAACCTGATCAGGACAGACCCACTCCAGTGTGGTCCACGTG 480	Qy	421	GGAGAGAAGTATGAACCTGATCAGGACAGACCCACTCCAGTGTGGTCCACGTG 480	Db	486	GGGAAAAGTGAATTGACCCAGGACTGACCAACTCCAGGCTGTTCCATGT 545
Qy	481	TCTGAGAGTGGCAAGAAGATGAGGAGAAGAGATGAGAATGAGAGACC 540	Qy	481	TCTGAGAGTGGCAAGAAGATGAGGAGAAGAGATGAGAATGAGAGACC 540	Db	546	TCTGAGAGTGGCAAGAAGAGATGAGGAGAAGAGATGAGAATGAGAGACC 602
Qy	541	AAGCCAAATCATCCAGAACAGGAGGACTACACCCATCCACCTTAGCTGA 597	Qy	541	AAGCCAAATCATCCAGAACAGGAGGACTACACCCATCCACCTTAGCTGA 597	Db	603	AAGCCAAATCATCCAGAACAGGAGGACTACACCCATCCACCTTAGCTGA 659
RESULT	13	ATGAAAGTTGTAATTGCTCAGACTTACACATAGGAAGTTCACACCTGGCTCGGCCAAAT 300	LOCUS	AK092184	AK092184 Homo sapiens cDNA FLJ34855 f1s, mRNA linear	PRI 15-JUL-2002		
DEFINITION		TO DOWN SYNDROME CRITICAL REGION PROTEIN 1.	DEFINITION	AK092184	AK092184 Homo sapiens cDNA FLJ34855 f1s, mRNA linear	highly similar		
ACCESSION			ACCESSION	AK092184_1	AK092184_1 GI:21750714			
VERSION		oligo capping; f1s (full insert sequence).	VERSION	518	CCAGACAAAGCAGTTCTGATCTCCCTCCGCCTCAGTGGATGGAAACAGTG	577		
KEYWORDS			KEYWORDS					

QY	361	GAAGATGCCACCCCGTATAAATTAGCATCTTATAGCCATCAGCTGGCCA	420		
Db	578	GAAGATGCCACCCCGTATAAACTATGATCTTATAGCCATCAGCTGGCCA	637		
QY	421	GGAGAGAATGAACTGTGAGCGAGAACCCACTCCAGTGTTGGCACCTG	480		
Db	638	GGGGAAAAGTATGAACTGTGAGCGAGCACCCACTCCAGTGTTGGCACATGTA	697		
QY	481	TGTGAGTGACCAAGAGATGAGGAGAGAGAGATGGGAGAATGAAAGACC	540		
Db	698	TGTGAGTGACCAAGAGATGGGAGAAGAGAAATGAGGAGAACCTG	754		
QY	541	AAGCCCAAATCATCCAGAACCGGAGACCGGAGTAGACACCGATCACCTAGCTGA	597		
Db	755	AAGCCCAAATATTCCAGACAGGAGGCCAGTACACGCCGATCACCTAGCTGA	811		
RESULT 14					
AB075973		626 bp mRNA linear	ROD 27-JUL-2002		
LOCUS		Rattus norvegicus mcip 1 mRNA for myocyte-enriched calcineurin-interacting protein 1, complete cds.			
DEFINITION					
ACCESSION	AB075973				
VERSION	1				
KEYWORDS					
SOURCE		Rattus norvegicus cDNA to mRNA.			
ORGANISM		Rattus norvegicus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
REFERENCE					
AUTHORS	Odashima,M., Nagata,K., Obata,K., Somura,F., Iizawa,H., Miyazaki,T., Murata,Y., Seo,H., Yamada,Y. and Yokota,M.				
TITLE	rat myocyte-enriched calcineurin interactant protein 1, splice variant 4 mRNA, complete cds				
JOURNAL	Odashima,M., Nagata,K., Obata,K., Somura,F., Iizawa,H., Miyazaki,T., Murata,Y., Seo,H., Yamada,Y. and Yokota,M.				
REFERENCE	2 (bases 1 to 626)				
AUTHORS	Obata,K., Nagata,K., Odashima,M., Somura,F., Yamada,Y. and Yokota,M.				
TITLE					
JOURNAL	Direct Submission				
Submitted [11-DEC-2001] Koji Obata, Nagoya University Department of Clinical Pathophysiology, 65 Tsurumi-cho, Showa-ku, Nagoya, Aichi 466-8550, Japan (E-mail:obata@esuru.med.nagoya-u.ac.jp, Tel:81-52-744-2577, Fax:81-52-744-2977)					
FEATURES	Location/Qualifiers				
source	1..626	/organism="Rattus norvegicus"			
gene	/db_xref="taxon:10116"				
CD5	1..626	/protein_id="BAC06443_1"			
CD5	/db_xref="GI:2199844"	/gene="mcip 1"			
CD5	/gene="mcip 1"	/translation="MHEFRDNFNSLIAVCANGDYSESETRAKFESLFRTYDKDT FQYKSFKEKVRINFSNPLSAADARLHLTEFLKEMKLYFAOHTHIGSSHLPENPD KQFSPSPPPVKGKPVYDYLAIKSLGPVYELHAATDTPSVWVHVH CESDDEEEEEEERMERMRKPKPKTQTRPEYPTPLS"			
BASE COUNT	182 a	163 c	154 g	127 t	
ORIGIN					
Query Match	72.28;	Score 430.8;	DB 10;	Length 626;	
Best Local Similarity	86.0%;	Pred. No. 2.9e-104;			
Matches	490;	Conservative			
		Mismatches 77;			
		Indels 3;			
		Gaps 1;			
gene					
CDS					
Qy	31	AGGCACCATCGCTGGCACTGGGCGGTTCTGTCAGCCCTGCGCC 90			
Db	49	AGCTCCGTGATGCCGAAACGGTATGCTTCAGGAAGCTCCAGTATTAGAC 150			
Qy	91	AAATTGAACTCCCTCTTCAAGACATATGACAGGACACCCCTTCAGATTTAAGAC 168			

```

/product="Adapt78"
/protein_id="AAB68517.1"
/db_xref="GI:2351391"
/translation="MIFRDENYNESSLIACYANGDVSESETRAKESLETFYDKIT
FOYFSKRVRINFSNPLSAARLQKEMKLYPAQLHIGSSHLAPPNPD
KOFKLISPPASPVGKROVEDATPVINYDLLVAISKLGPERKELHAATDTPSVYHV
CESDQENEEEEMERAKRKPKEIIGPRPEVPIHLUS"

```

BASE COUNT ORIGIN	544	a	564	g	593	t			
Query Match	71.7%	Score	427.8	DB 10;	Length	2216;			
Best Local Similarity	85.9%	Pred. No.	2.1e-103;						
Matches	487;	Conservative	0;	Mismatches	77;	Indels	3;	Gaps	1;

Qy	31	AGGCCACCATCCCTGCCACCTGGACCGCGGGTGTGACGCCCTGCGGCC	90
Db	100	AGTCCCCCTGATTCGCTGTTGCAAACGGTGTGCTTCAGGAAAGTGAAACCAGGGC	159
Qy	91	AATTTGAATCCCCTCTTCAAAATCATACAAGAACACCACTTCCACTATTAAAGAC	150
Db	160	AATTTGAATCCCCTCTTCAAGGAGTATCACATTCAGTATTAAGAC	219
Qy	151	TTCAAACGTTGTCGGATAAAACTTCAGCAAACCCCTTATCTGCCAGGTGCGG	210
Db	220	TTCAAACGTTGCCAAATTCAGCAAACCCCTTATCTGCCAGGTGCGG	279
Qy	211	CTGCACAAAGCCAGTTCCTGGGAAGGAANGAAGTGTATTTCAGTACTTTAAC	270
Db	280	CTGCATAAAGACSGAGTTCCTGGGAAGGAATGAAGCTGACTTTGCTCAGCGTTAAC	339
Qy	271	ATAGGAAGTTCAACCTGGTCGCCCAATCCCGACAAACGTTCCCTCATCTCCCTCCG	330
Db	340	ATAGGAAGCTCACACCTGGTCGCCCAATCCAGACAGCAGTCCCTCATCTCCCTCC	399
Qy	331	GCCTCTCTCCGTTGGCTGGAAACAACAGTAGAAGATGCAACCCCGTCATAATTAGAT	390
Db	400	GCCTCTCCACCACTGGTGGAGCAAGTAGAACGCTAACCCCAAGTCATAATTACAT	459
Qy	391	CTTTATATGCCATCTCAAGCTGGGCCAGGAGAAGTGAACCTGATGCCAGCACA	450
Db	460	CTTTATATGCCATCTCAAGCTGGGCCAGGAGAAGTGAACGCTGATGCCAGCACA	519
Qy	451	GACCCACTCCCAAGTGTGTCACCTGTGTGAGAGTGAACAGAATGAGGAGGA	510
Db	520	GACACCCTCCCAAGTGTGTCACCTGTGTGAAAGCAGCAAGAATGAGGAGGA	576
Qy	511	GAGGAAGAGATGGAGAATGAGAGAGACCAAGCCAAAATCATCCAGAACGGAGAC	570
Db	577	GAGGAGGAGATGGAGAATGAGAGACCAAGCCAAAATCATCCAGAACGGAGGCA	636
Qy	571	GAGTACACCGATCCACCTTAGCTGA	597
Db	637	GAGTACACGGCTATCCACCTAGCTGA	663

Search completed: November 15, 2002, 02:55:35  
Job time : 2658 secs

*THIS PAGE BLANK (23970)*

Nucleotide sequence  
Human Down Syndrom  
Human secreted protein  
Human MCIP associa  
Collagen  
Lung cancer relate  
Human MCIP associa  
Human MCIP associa  
Human MCIP associa  
Rat Down syndrome  
Mouse MCIP associa  
Human foetal liver  
Human brain expres  
Probe #4382 for ge  
Probe #4382 used t  
Probe #4263 used t  
Human genome-deriv  
Human breast cell  
Human foetal liver  
Probe #2064 for ge  
Human brain expres  
Human bone marrow  
Human foetal liver  
Probe #2081 for ge  
Probe #2179 used t  
Probe #2052 used t  
Human genome-deriv  
Rat Down syndrome  
Human breast cell  
Human foetal liver  
Probe #809 for gen  
Human brain expres  
Human bone marrow  
Probe #836 for gen  
Probe #849 used to  
Probe #816 used to  
Human genome-deriv  
Human colon cancer

10 211 35.3 934 22 AAF25338  
11 211 35.3 3159 24 ABA1457  
12 207 34.7 442 21 AAC0174  
13 193 32.3 3184 24 AAD30157  
14 193 32.3 3184 24 ABL61768  
15 193 32.3 3184 24 ABL6187  
16 186.4 31.2 720 24 AAD30159  
17 186.4 31.2 828 24 AAD30158  
18 184.6 30.9 615 24 ABA9463  
19 183 30.7 594 24 AAD30154  
c 20 144.6 24.2 412 22 ABA5172  
c 21 144.6 24.2 412 22 AAK0364  
c 22 144.6 24.2 412 22 AAI14449  
c 23 144.6 24.2 412 22 AAI5821  
c 24 144.6 24.2 412 22 AAI0272  
c 25 144.6 24.2 412 24 ABB0419  
c 26 144.6 24.2 446 22 ABA3406  
c 27 144.6 24.2 446 22 ABA53852  
c 28 144.6 24.2 446 22 ABA23598  
c 29 144.6 24.2 446 22 AAK02113  
c 30 144.6 24.2 446 22 AAK27563  
c 31 144.6 24.2 446 22 AAI12148  
c 32 144.6 24.2 446 22 AAI3493  
c 33 144.6 24.2 446 22 AAI02061  
c 34 136.6 24.2 446 22 AAI02041  
c 35 136.6 22.9 1021 24 ABA91458  
c 36 123 20.6 486 22 ABA2132  
c 37 123 20.6 486 22 ABA52554  
c 38 123 20.6 486 22 ABA22343  
c 39 123 20.6 486 22 AAK00816  
c 40 123 20.6 486 22 AAK26270  
c 41 123 20.6 486 22 AAI10903  
c 42 123 20.6 486 22 AAI3163  
c 43 123 20.6 486 22 AIO0825  
c 44 123 20.6 486 24 ABS00858  
c 45 94.4 15.8 640 24 ABQ59719

## ALIGNMENTS

RESULT 1

ID AAD30152 standard; DNA; 597 BP.

1: N\_Geneseq\_101002:  
 2: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1980.DAT:  
 3: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1981.DAT:  
 4: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1982.DAT:  
 5: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1983.DAT:  
 6: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1984.DAT:  
 7: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1985.DAT:  
 8: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1986.DAT:  
 9: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1987.DAT:  
 10: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1988.DAT:  
 11: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1989.DAT:  
 12: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1991.DAT:  
 13: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1992.DAT:  
 14: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1993.DAT:  
 15: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1994.DAT:  
 16: /SIDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA1995.DAT:  
 17: /SIDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA1996.DAT:  
 18: /SIDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA1997.DAT:  
 19: /SIDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA1998.DAT:  
 20: /SIDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA1999.DAT:  
 21: /SIDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA2000.DAT:  
 22: /SIDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA2001A.DAT:  
 23: /SIDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA2001B.DAT:  
 24: /SIDS2/gcgdata/geneseq/geneseq/geneseq/geneseq-emb1/NA2002.DAT:

Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;  
heart failure; cardiomyopathy; heart disease; human; gene; ds.  
Homo sapiens.

WO200204491-A2.

Location/Qualifiers

/\*tag= a

/product= "Human MCIP associated protein #2"

## SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	597	100.0	597	24	AAD30152	Human MCIP associa
2	515.8	86.4	597	24	AAD30153	Mouse MCIP associa
3	481.8	80.7	2212	24	AAD30156	Human MCIP associa
4	469	78.6	2358	21	AAF18328	Lung cancer associ
5	426.2	71.4	599	24	AAD30151	Human MCIP associa
6	403.8	67.6	2331	24	AAD30155	Human MCIP associa
7	399.6	66.9	2173	24	ABN96843	Gene #3341 used to
8	398	66.7	2174	20	AAO1282	Human DSCR1 coding
9	392.8	65.8	2348	24	AAS94805	Human DNA sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

8

Result No.	Score	Query	Match Length	DB	ID	Description
1	597	100.0	597	24	AAD30152	Human MCIP associa
2	515.8	86.4	597	24	AAD30153	Mouse MCIP associa
3	481.8	80.7	2212	24	AAD30156	Human MCIP associa
4	469	78.6	2358	21	AAF18328	Lung cancer associ
5	426.2	71.4	599	24	AAD30151	Human MCIP associa
6	403.8	67.6	2331	24	AAD30155	Human MCIP associa
7	399.6	66.9	2173	24	ABN96843	Gene #3341 used to
8	398	66.7	2174	20	AAO1282	Human DSCR1 coding
9	392.8	65.8	2348	24	AAS94805	Human DNA sequence

Result No.	Score	Query	Match Length	DB	ID	Description
1	597	100.0	597	24	AAD30152	Human MCIP associa
2	515.8	86.4	597	24	AAD30153	Mouse MCIP associa
3	481.8	80.7	2212	24	AAD30156	Human MCIP associa
4	469	78.6	2358	21	AAF18328	Lung cancer associ
5	426.2	71.4	599	24	AAD30151	Human MCIP associa
6	403.8	67.6	2331	24	AAD30155	Human MCIP associa
7	399.6	66.9	2173	24	ABN96843	Gene #3341 used to
8	398	66.7	2174	20	AAO1282	Human DSCR1 coding
9	392.8	65.8	2348	24	AAS94805	Human DNA sequence

(ROTH/)

ROTHMERL B.

(TEXA ) UNIV TEXAS SYSTEM.

(WILL/ ) WILLIAMS S R.

RESULT 2  
 AAD30153 standard; DNA: 597 BP.

XX PI Williams SR, Rothermel B;

XX DR WPI; 2002-179698/23.

DR P-PSDB; AAE18911.

XX Screening for modulators of muscle calcineurin interacting protein (MCIP) binding, expression or phosphorylation, useful for treating cardiac hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a test compound -

XX PS Claim 95; Page 147-148; 174pp; English.

XX The invention relates to muscle calcineurin interacting proteins (MCIPs) and nucleic acid molecules encoding such proteins. MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin to stimulate transcription of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for treating cardiac hypertrophy and heart failure. Antibodies to MCIP can be used in characterising the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomopathy or as predictor of heart disease.

XX The present sequence is human MCIP associated DNA.

XX Sequence 597 BP; 160 A; 170 C; 151 G; 116 T; 0 other;

Query Match Score 597; DB 24; Length 597;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-169;  
 Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ATGGAGGGAGGTGATCTCGAGGACCTCGCCAGGCCACCATCGCTGCCCCACCTGGACCCG 60

Db 1 ATGGAGGGAGGTGATCTCGAGGACCTCGCCAGGCCACCATCGCTGCCCCACCTGGACCCG 60

Qy 1 CCGGTGTCGTGACGGCCTCGCCGGCAAAATTGAACTCCCTCTCAGAACATATGAC 120

Db 61 CCGGTGTCGTGACGGCCTCGCCGGCAAAATTGAACTCCCTCTCAGAACATATGAC 120

Qy 121 AGGACACCCACTTCCAGATTATTAAAGAGCTTCAAAAGTGTCTCGGGATAAACTTCAGCAAC 180

Db 61 CCGCTGTCGTGACGGCCTCGCCGGCAAAATTGAACTCCCTCTCAGAACATATGAC 120

Qy 121 AGGACACCCACTTCCAGATTATTAAAGAGCTTCAAAAGTGTCTCGGGATAAACTTCAGCAAC 180

Db 181 CCCATTATCGAGCGATGCCAGGTGGCTGACAGACCGAGTTCTGGGAAAGGA 240

Qy 181 CCCATTATCGAGCGATGCCAGGTGGCTGACAGACCGAGTTCTGGGAAAGGA 240

Db 181 CCCATTATCGAGCGATGCCAGGTGGCTGACAGACCGAGTTCTGGGAAAGGA 240

Qy 241 ATGAAGTTGTTATTGCTGAGCTTACATAGGAAGTTCACACCTGGCTCGCCCAAT 300

Db 241 ATGAAGTTGTTATTGCTGAGCTTACATAGGAAGTTCACACCTGGCTCGCCCAAT 300

Qy 301 CCCGACAAACAGTGTCTCATCTCCCCTCGGCCCTCTCCCTGGCTGGTGGAAACAGTA 360

Db 301 CCCGACAAACAGTGTCTCATCTCCCCTGGCTGGTGGAAACAGTA 360

Qy 361 GAAGATGCCACCCCGTCATAAATTACGATCTCCAGCTGGCTGGTGGAAACAGTA 420

Db 361 GAAGATGCCACCCCGTCATAAATTACGATCTCCAGCTGGCTGGTGGAAACAGTA 420

Qy 421 GGAGAGAAGTGAATGGAATGGAATGGAGGAAGATGGAGATGAAGAGACC 480

Db 421 GGAGAGAAGTGAATGGAATGGAATGGAGGAAGATGGAGATGAAGAGACC 480

Qy 481 TGTGAGAGTGAATGGAATGGAGGAAGATGGAGATGAAGAGACC 540

Db 481 TGTGAGAGTGAATGGAATGGAGGAAGATGGAGATGAAGAGACC 540

Qy 541 AAGCCCAAATCATCCAGACGGAGACGGAGTACACACCGATCCACCTTAGCTGA 597

Db 541 AAGCCCAAATCATCCAGACGGAGACGGAGTACACACCGATCCACCTTAGCTGA 597

XX Sequence 597 BP; 170 A; 156 C; 142 G; 129 T; 0 other;

Query Match Score 86.4%; Score 515.8; DB 24; Length 597;  
 Best Local Similarity 94.4%; Pred. No. 3.3e-145;  
 Matches 535; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 31 AGCGCACCATCGCTGCCACCTGGACCGCGCTTCTGTCGAGGGGGCC 90

Db 31 AGCTCCCTGATGCTTGTCGCCAACAGATGTCCTGGCAAGTGCAGACGGGCC 90

Qy 91 AAATTGAATCCCTCTCAGAACATATGACAAGGACACCACTTCAGTATTAAAGAC 150

.r<sub>t</sub>

Db 91 AAATTGAAATCCCTCTTCAGAACATATGACAAGAACCAACCTTCCAGTATTAAAGACC 150  
 Qy 151 TICAAACGTGTCGGATAAACTTCACAAACCCCTATCTGAGCCATGCCATGGCTGG 210  
 Db 151 TTCAACGTGTCGGATAAACTTCACAAACCCCTATCTGAGCCATGCCATGGCTGG 210  
 Qy 211 CTGACAAAGACCGAGTCTGGGAAGAAATGAAGCTTGTATTTCTCAGACTTACAC 270  
 Db 211 CTGACAAAGACCGAGTCTGGGAAGAAATGAAGCTTGTATTTCTCAGACTTACAC 270  
 Qy 271 ATAGGAAGTTCACACCTGGCTCGGCCAAACAGTTCCTCATCTCCCTCCG 330  
 Db 271 ATAGGAAGTTCACACCTGGCTCGGCCAAACAGTTCCTCATCTCCCTCCG 330  
 Qy 331 GCCTCTCTCCCGTGGTGGTGGAAACAGTAGAAAGATGCCACCCCCATAAATTACGT 390  
 Db 331 GCCTCTCTCCCGTGGTGGTGGAAACAGTAGAAAGATGCCACCCCCATAAATTACGT 390  
 Qy 391 CTTTATATGCCATCTCAAGCTGGGCCAGAGAATGAACTGCATGCAGCGACA 450  
 Db 391 CTTTATATGCCATCTCAAGCTGGGCCAGAGAATGAACTGCATGCAGCGACA 450  
 Qy 451 GACCCACTCCCACTGGTGGTCCACGTGGTGGAGTGGCAAGAGATGAGGGAA 510  
 Db 451 GACCCACTCCCACTGGTGGTCCACGTGGTGGAGTGGCAAGAGATGAGGGAA 510  
 Qy 511 GAGGAAGAGATGGAGAAATGAAGAACCCAAAGCCAAAGATGAGGGAAACCG 570  
 Db 511 GAGGAAGAGATGGAGAAATGAAGAACCCAAAGCCAAAGATGAGGGAAACCG 570  
 Qy 571 GAGTACACCCGATCCACCTTAGCTGA 597  
 Db 571 GAGTACACCCGATCCACCTTAGCTGA 597

RESULT 3

AAD30156 ID AAD30156 standard; DNA; 2212 BP.

XX AC AAD30156;

XX DT 17-MAY-2002 (first entry)

XX DE Human MCIP associated DNA #2.

XX KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy; heart failure; cardiomyopathy; heart disease; human; gene; ds.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FH 25..618 /\*tag= a /product= "Human MCIP associated protein #2"

FT PN WO200204491-A2.

XX PD 17-JAN-2002.

XX PF 06-JUL-2001; 2001WO-US21662.

XX PR 07-JUL-2000; 2000US-216601P.

PR 13-FEB-2001; 2001US-0782953.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

PA (WILL,/ ) WILLIAMS S. R.

PA (ROTHMEL/ ) ROTHERMEL B.

XX PI Williams SR, Rothermehl B;

XX DR WPI: 2002-179698/23.

DR P-PSDB; AAE18915.

PT Screening for modulators of muscle calcineurin interacting protein (MCIP) binding, expression or phosphorylation, useful for treating cardiac hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a test compound -

XX Example 1; Page 159-161; 174pp; English.

CC The invention relates to muscle calcineurin interacting proteins (MCIPs) and nucleic acid molecules encoding such proteins. MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin to stimulate transcription of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for treating cardiac hypertrophy and heart failure.

CC Antibodies to MCIP can be used in characterising the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomyopathy or as predictor of heart disease.

CC The present sequence is human MCIP associated DNA.

CC Note: This sequence has been described as murine MCIP splice variant in the specification, however the sequence seems to be a polynucleotide encoding a MCIP associated protein.

XX Sequence 2212 BP; 588 A; 455 C; 529 G; 640 T; 0 other;

Query Match 80.7%; Score 481.8; DB 24; Length 2212;

Best Local Similarity 89.1%; Pred. No. 1..le-134; Indels 3; Gaps 1;

Matches 532; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

Qy 1 ATGGAGGAGGTGGATCTGGAGACCTGCGAGGGCACCATGCCCTCCACGTGACCG 60

Db 25 ATGGAGGAGGTGGACTCTGGAGAACCTGCCAGGGCACCATGCCCTCCACGTGACCG 84

Qy 61 CGCGTGTTCTGTGAGCGCTCTGCGCCAAATTGTAATCTCAGACATATGAC 120

Db 85 CGGGTGTTCTGTGAGCGCTCTGCGCCAAATTGTAATCTCAGACATATGAC 144

Qy 121 AAGGACACCACCTTCAGTATTAGAGCTTCAAAGGTGTCGGATAACTTCAGAAC 180

Db 145 AAGGACATCACCTTCAGTATTAGAGCTTCAAAGAGTCAAGATAAACCTCAGAAC 204

Qy 181 CCCTTATGTGAGCCGATGCCAGGTGGCGCACAAAGCCGAGTCTGGGAAGGAA 240

Db 205 CCCTTCTCCGAGGAGATGCCAGGTGGCGCATTAAGACTGAGTTCTGGAAAGGAA 264

Qy 241 ATGAAAGTGTATTGTGCTCAGACTTACATAGGAAGTCTACAGACTTACAC 300

Db 265 ATGAAAGTGTATTGTGCTCAGACTTACACAGAACTGAGCTGGCTGGCAAAAT 324

Qy 301 CCCGACAAACAGTTCTCATCTCCCGCTCTCCCGTGGCTGGAAACAGTA 360

Db 325 CCAGACAAAGCAGTTCTGATCCCTCCCTCCGCTCTCCGCAAGTGGATGAAACAGTG 384

Qy 361 GAGATGGCACCCCGTCATAATTAGATCPTTTATGCATCTCAAGCTGGGCCA 420

Db 385 GAGATGGCACCCCGTCATAATTAGATCPTTTATGCATCTCAAGCTGGGCCA 444

Qy 421 GGAGGAGGTGAAATGAGTCAAGAACGGAGACCCAGTCAGCTGGCTGGCAAT 480

Db 445 GGGAAAGATGATGAACTGACCCAGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 504

Qy 481 TGAGAGTGTGAAATGAGTCAAGAACGGAGACCCAGTCAGCTGGCTGGCTGGCTGG 540

Db 505 TGAGAGTGTGAAATGAGTCAAGAACGGAGACCCAGTCAGCTGGCTGGCTGGCTGG 561

Qy 541 AGGCCAAAATCATCAGAACGGAGTACACGGATCAACCTTGTGCTGA 597

Db 562 AAGCCAAAATPATCAGACCCAGTCAGCCGATCACCTCAGCTCACCTCAGCTGA 618

RESULT 4

AAF18328 ID AAF18328 standard; DNA; 2358 BP.



CC transcription of certain target genes. The invention also relates to  
 CC methods for identifying modulators of MCIP binding, expression or  
 CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin  
 CC may be used for treating cardiac hypertrophy and heart failure.  
 CC Antibodies to MCIP can be used in characterising the MCIP content of  
 CC healthy and diseased tissues and subsequently for determining the  
 CC presence or absence of cardiomyopathy or is predictor of heart disease.  
 CC The present sequence is human MCIP associated DNA.

xx Sequence 599 BP; 164 A; 150 C; 149 G; 136 T; 0 other;  
 Query Match 71.4%; Score 426.2; DB 24; Length 599;  
 Best Local Similarity 93.1%; Pred. No. 3. 4e-118;  
 Matches 457; Conservative 0; Mismatches 33; Indels 1; Saps 1;

Qy 31 AGGCCACCATCGCCCTGGCACCTGGGCGGTGTTGAGCAGCGCTTGCGGGCC 90  
 Db 110 AGCTCCCTGATGCTGCTGATGATGATGCTTCAGCAAAAGTGAGAACAGGGC 169  
 Qy 91 AAATTGAAATCCCTCTCTAGAACATATGACAAGGACACCCTCCAGTATTAGAGC 150  
 Db 170 AAATTGAAATCCCTCTCTAGAACATATGACAAGGACACCCTCCAGTATTAGAGC 229  
 Qy 151 TCCAACGTGTCGGATAAATTCAAGAACCCCTTATCTGAGCCGATGCCGGTGG 210  
 Db 230 TCCAACGTGTCGGATAAATTCAAGAACCCCTTATCTGAGCCGATGCCGGTGG 289  
 Qy 211 CTGCACRAAGACGGAGTCTCTGGGAAGAAATGAAACTTGATGAACTTCTCAC 270  
 Db 290 CTGCACRAAGACGGAGTCTCTGGGAAGAAATGAACTTGATGAACTTCTCAC 349  
 Qy 271 ATAGGAAGTTCACACCTGGCCTGGCCAAATCCGAAACAGTCCCTCATCCCTCG 330  
 Db 350 ATAGGAAGTTCACACCTGGCCTGGCCTGGGAACACAGTCTCCATCTCCCTCG 408  
 Qy 331 GCCTCCTCCCGTGGTGGTGGTGGAAACAGTAGAGATGCCACCCCGTCATAATTAGAT 390  
 Db 409 GCCTCCTCCCGTGGTGGTGGAAACAGTAGAGATGCCACCCCGTCATAATTAGAT 468  
 Qy 391 CTTTATATGGCATTCTCAAGTGGCCGCAAGTGGAGAGATGAACTGAGGACA 450  
 Db 469 CTTTATATGGCATTCTCAAGTGGCCGCAAGTGGAGAGATGAACTGAGGACA 528  
 Qy 451 GACCCCACTCCAGTGGTGGTCCACGTGTTGAGATGCCAAGAGATGAGGAGGA 510  
 Db 529 GACACCACTCCAGTGGTGGTGGTCCACGTGTTGAGATGCCAAGAGATGAGGAGGA 588  
 Qy 511 GAGGAAGAGAT 521  
 Db 589 GAGGAAGAGAT 599

RESULT 6  
 ADD30155 DT 17-MAY-2002 (first entry)  
 XX ID ADD30155 standard; DNA; 2331 BP.  
 XX DE Human MCIP associated DNA #1.  
 XX AC ADD30155;  
 OS Homo sapiens.  
 XX FH Location/Qualifiers  
 FT 144..737 /\*tag= a  
 FT /product= "Human MCIP associated protein #1"  
 XX WO200204491-A2.

xx Sequence 2331 BP; 630 A; 470 C; 547 G; 684 T; 0 other;  
 Qy 31 AGGCACCATCGCCCTGGCACCTGGGCGGTGTTGAGCAGCGCTTGCGGGCC 90  
 Db 174 AGTCCTGATGCTGCTGATGATGATGCTTCAGCAAAAGTGAGAACAGGGC 233  
 Qy 91 AAATTGAAATCCCTCTCTAGAACATATGACAAGGACACCCTCCAGTATTAGAGC 150  
 Db 234 AAATTGAAATCCCTCTAGAGCTATGAACTGAGATATTCAGCAAAAGTGAG 293  
 Qy 151 TTCAAACGTGTCGGATAAATTCAAGAACCCCTTATCTGAGCCGATGCCGGTGG 210  
 Db 294 TTCAAACGTGTCGGATAAATTCAAGAACCCCTTATCTGAGCCGATGCCGGTGG 353  
 Qy 211 CTGCACAAAGACGGAGTCTCTGGGAAGAAATGAACTTGATGTCAGCTTACAC 270  
 Db 354 CTGCATATAGACTGAGCTGTTCTGGAAAGAAATGAGTTTGGCTCAGCTTACAC 413  
 Qy 271 ATAGGAAGTTCACCTGGCTCGCCAAATCCGAAACAGTTCATCTCCCTCG 330  
 Db 414 ATAGGAAGTTCACCTGGCTCGCCAAATCCGAAACAGTTCATCTCCCTCG 473  
 Qy 331 GCCTCCTCCGGTGGGAAAGAACAACTGAGATGCCACCCCGTCATAATTAGAGC 390  
 Db 474 GCCTCCTCCGGTGGGAAAGAACAACTGAGATGCCACCCCGTCATAATTAGAGC 533  
 Qy 391 CTTTATATGGCATTCTCAAGAACAGTGGCTGGGGCAGGAGAAGATGAACTGCA 450  
 Db 534 CTTTATATGGCATTCTCAAGAACAGTGGCTGGGGCAGGAGAAGATGAACTGCA 593

xx 17-JAN-2002.  
 PD 06-JUL-2001; 2001WO-US21662.  
 PF 07-JUL-2000; 2000US-216601P.  
 PR 13-FEB-2001; 2001US-0782953.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (WILL/ ) WILLIAMS S R.  
 PA (ROTH/ ) ROTHERMEL B.  
 PI Williams SR, Rothermel B;  
 XX DR 2002-179698/23.  
 DR P-PSDB; AAE1B914.

xx Screening for modulators of muscle calcineurin interacting protein (MCIPs) (MCIPs) for modulators of muscle calcineurin interacting protein (MCIPs) (MCIP) binding, expression or phosphorylation, useful for treating cardiac hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a test compound -  
 XX Claim 72; Page 155-157; 174pp; English.  
 XX The invention relates to muscle calcineurin interacting proteins (MCIPs). MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin to stimulate transcription of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for creating cardiac hypertrophy and heart failure. Antibodies to MCIP can be used in characterising the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomopathy or as predictor of heart disease. Note: This sequence has been described as a promoter in claim 72 of the specification, however the sequence seems to be a polynucleotide encoding a MCIP associated protein.

XX DR 2002-179698/23.  
 XX DR P-PSDB; AAE1B914.  
 XX PT Screening for modulators of muscle calcineurin interacting protein (MCIPs) (MCIP) binding, expression or phosphorylation, useful for treating cardiac hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a test compound -  
 XX PS Claim 72; Page 155-157; 174pp; English.  
 XX The invention relates to muscle calcineurin interacting such proteins. MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin to stimulate transcription of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for creating cardiac hypertrophy and heart failure. Antibodies to MCIP can be used in characterising the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomopathy or as predictor of heart disease. Note: This sequence has been described as a promoter in claim 72 of the specification, however the sequence seems to be a polynucleotide encoding a MCIP associated protein.

XX SQ Sequence 2331 BP; 630 A; 470 C; 547 G; 684 T; 0 other;  
 Qy 31 AGGCACCATCGCCCTGGCACCTGGGCGGTGTTGAGCAGCGCTTGCGGGCC 90  
 Db 174 AGTCCTGATGCTGCTGATGATGATGCTTCAGCAAAAGTGAGAACAGGGC 233  
 Qy 91 AAATTGAAATCCCTCTCTAGAACATATGACAAGGACACCCTCCAGTATTAGAGC 150  
 Db 234 AAATTGAAATCCCTCTAGAGCTATGAACTGAGATATTCAGCAAAAGTGAG 293  
 Qy 151 TTCAAACGTGTCGGATAAATTCAAGAACCCCTTATCTGAGCCGATGCCGGTGG 210  
 Db 294 TTCAAACGTGTCGGATAAATTCAAGAACCCCTTATCTGAGCCGATGCCGGTGG 353  
 Qy 211 CTGCACAAAGACGGAGTCTCTGGGAAGAAATGAACTTGATGTCAGCTTACAC 270  
 Db 354 CTGCATATAGACTGAGCTGTTCTGGAAAGAAATGAGTTTGGCTCAGCTTACAC 413  
 Qy 271 ATAGGAAGTTCACCTGGCTCGCCAAATCCGAAACAGTTCATCTCCCTCG 330  
 Db 414 ATAGGAAGTTCACCTGGCTCGCCAAATCCGAAACAGTTCATCTCCCTCG 473  
 Qy 331 GCCTCCTCCGGTGGGAAAGAACAACTGAGATGCCACCCCGTCATAATTAGAGC 390  
 Db 474 GCCTCCTCCGGTGGGAAAGAACAACTGAGATGCCACCCCGTCATAATTAGAGC 533  
 Qy 391 CTTTATATGGCATTCTCAAGAACAGTGGCTGGGGCAGGAGAAGATGAACTGCA 450  
 Db 534 CTTTATATGGCATTCTCAAGAACAGTGGCTGGGGCAGGAGAAGATGAACTGCA 593

QY	88	GCCAAATTGATCCTCTTCAGACAGGACACCCTTCAAGATTTAG	147
Db	58	GCCAAATTGATCCTCTTCAGACAGGACACCCTTCAAGATTTAG	117
OY	148	ACGTCAACAGTGTGGATAACTTCAGAACCCCTATCTGCAGGCCATGGCGTC	207
Db	118	ACCTCAACAGTGTGGATAACTTCAGAACCCCTATCTGCAGGCCATGGCGTC	177
QY	208	CGGCTGACAAGACCGAGTCTGGGAAGGAATTGAAGTGTATTTGTCAGACTTAA	267
Db	178	CACTGATAAGACTGATTCGGAAAGGAATAAGTTATTTGTCAGACCTTA	237
QY	268	CACATAGGAAGTCACCTGTCACCTGTCATCCGACAGGATTCAGCTCCCT	327
Db	238	CACATAGGAAGTCACCTGTCACCTGTCATCCGACAGGATTCAGCTCCCT	297
QY	328	CCGGCCTTCCTCCGTTGGCAACAGTAGATGCGACCCCCCTCATAAATTAC	387
Db	298	CCGGCCTTCCTCCGCACTGGGATGAACTGGACCCAGTCATAAATCAT	357
QY	388	GATCTTTATATGCCATTCGAGCTGGCCAGAGAAGTAACTGCATGCAGCG	447
Db	358	GATCTCTATATGCCATTCGAGCTGGCCAGAGAAGTAACTGCAGCG	417
QY	448	ACGACCCCACTCCAGCTGGCCAGAGAAGTAACTGCATGCAGCG	507
Db	418	ACTACACCCACTCCAGCTGGGTCATGTTGAGTGTCAAGAGAGGAA	477
QY	508	GAAAGGAGAGATGGAGAATGAAAGAGCCAAATCATCGACACGCGAGA	567
Db	478	GAAGAGAA---AGGAAGAATGGAGACCTAGCTGGCCAGGGAAAGT	534
QY	568	CGGAGTACACCGATCCACCTTGCTGA	597
Db	535	CGGAGTACACGGATCCACCTTGCTGA	564
RESULT 7			
D	ABN96843	standard; DNA; 2173 BP.	
C	ABN96843;		
C		13-AUG-2002 (first entry)	
E		Gene #3341 used to diagnose liver cancer.	
X		Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.	
X		Homo sapiens.	
X	W0200229103-A2.		
X	11-APR-2002.		
X	02-OCT-2001; 2001WO-US30589.		
X	02-OCT-2000; 2000US-237054P.		
X	(GENE-) GENE LOGIC INC.		
X	Horne D, Alvares C, Peres-Da-Silva S, Vockley JG.		
X	WPI: 2002-426119/45.		
X	Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample -		
X	Claim 1: SEQ ID NO 3341; 298pp; English.		
X	The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN9745 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.		
X	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <a href="http://wipo.int/pub/published_pct_sequences">ftp://wipo.int/pub/published_pct_sequences</a> .		
ES	Sequence 2173 BP; 606 A; 431 C; 503 G; 633 T; 0 other;		
ES	Query Match 66.9%; Score 399.6; DB 24; Length 2173;		
ES	Best Local Similarity 87.8%; Ped. No. 6.6e-10;		
ES	Mismatches 0; Conservative 0; Gaps 3; Indels 59;		
XX	(PALL/) PALLEJA X E.		
XX	XX		
PA	Fuentes JJ, Palleja XE, Pritchard M;		
PI			
XX	WPI: 1999-152781/13.		
DR			



601	TGACACCCTCCACCGTGGTCATGTATGAGAGAGAA	660	XX	Sequence	934	BP;	247	A;	244	C;	206	G;	237	T;	0	other;
510	AGAGGAAGAGATGGAGAGATAAGAACCCAAAATCATCCAGCACGGAGACC	569	XX	Query Match	35	:38	:	Score	211:	DB	22:	Length	934:			
661	AGAGGA--ATTGAAAGATAAGGGACCTAAGGCCAAAATTCCAGCCAGGGCC	717	Db	Best Local Similarity	65	:28	:	Pred.	No.	3..1e-5;						
570	GGAGTACACCGTACCGTACCCCTAGCTGA	597	Qy	Matches	332;	Conservative	0;	Mismatches	165;	Indels	12;	Gaps	1:			
718	GGAGTACACGCCGATCCACCTCAGCTGA	745	Db	143	GACTTAATGACCTCCCACACTGTGTTGTCAGTGTGAA	202										
RESULT 10																
LD	AAF25338	standard;	CDNA;	934	BP.											
	AAF25338;															
30-APR-2001 (first entry)																
Nucleotide sequence of a human detoxification protein.																
Human; detoxification protein; DETX; cancer; leukaemia; melanoma; adenocarcinoma; autoimmune disorder; inflammatory disorder; rheumatoid arthritis; asthma; atherosclerosis; autoimmune thyroiditis; psoriasis; ulcerative colitis; infection; cell proliferative disorder; actinic keratosis; arteriosclerosis; cirrhosis; hepatitis; ss.																
Homo sapiens.																
Key																
CDS	20..724															
	/tag=	a														
	/product=	"detoxification protein"														
s19_peptide	20..100															
	/tag=	b														
WO200104305-A2.																
18-JAN-2001.																
06-JUL-2000; 2000WO-US18509.																
07-JUL-1999; 99US-0142678.																
(INCY-) INCYTE GENOMICS INC.																
Tang YT, Yue H;																
WPI; 2001-147193/15.																
P-PSDB; AAB31788.																
New human detoxification protein and polynucleotide, useful for diagnosis, prevention and treatment of autoimmune/inflammatory disorders and cell proliferative disorders including cancer -																
Claim 5; Page 79; 79pp; English.																
The present sequence encodes a human detoxification polypeptide (DETX). DETX and its (ant)agonists are useful for preventing or treating disorders associated with decreased or increased expression or activity of DETX. DETX polypeptides are useful for screening compounds that specifically binds to DETX and for identifying (ant)agonists. Diseases prevented, treated and diagnosed include cancers (e.g. leukaemia, melanoma, adenocarcinoma, cancers of the brain, bone marrow, breast, kidney, liver, pancreas, prostate and uterus), autoimmune/inflammatory disorders (e.g. rheumatoid arthritis, asthma, atherosclerosis, autoimmune thyroiditis, psoriasis and ulcerative colitis), bacterial, fungal, parasitic infections and cell prolifertive disorders (e.g. actinic keratoses, arteriosclerosis, cirrhosis and hepatitis). Anti-DETX antibodies may be used as antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into contact with cells or tissues expressing DETX and for diagnosis of DETX related disorders.																
CC																
CC																
CC																
CC																
CC																
CC																
CC																
CC																
CC																
CC																
CC																
CC																
CC																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																
XX																

XX	PR 11-JUL-2000; 2000US-0614474.	Db 791 GGAGGAAGTATGACTCCATGGAGGGACTGACCCCCAAGTCACCTGCCTCGTCACCTG 850
XX	PA (INCYT-) INCYTE GENOMICS INC.	QY 481 TGTGAGAGTGACCAAGAGATGAGGAGGA 509
XX	PT Loring JF, Tingley DW, Edwards CM, Streeter DG;	DB 851 TGCCACAGTGACATGAGGAAGAGAGGA 879
XX	DR WPI; 2002-164633/21.	RESULT 12
XX	DR P-PSDB; AAM50760.	AAC01774 ID AAC01774 standard; cDNA; 442 BP.
XX	PT Novel Down syndrome critical region 1-like 1 protein and nucleic acid encoding the protein useful for diagnosis and treatment of Alzheimer's disease, Down syndrome and other forms of dementia	Novel secreted protein 5' EST, SEQ ID NO: 1772.
XX	PS Claim 2; Page 46-47; 54pp; English.	XX Human secreted protein 5' EST, SEQ ID NO: 1772.
XX	CC The present sequence is that of cDNA clone Incyte ID No: 247500.5 encoding novel Down syndrome critical region 1-like 1 protein (DSCR1L alpha, see AAM50760). Northern analysis indicated expression of DSCR1L alpha in various libraries, with the highest abundance in tissues from the nervous system, including tissues associated with schizophrenia, Huntington's disease, epilepsy and amyotrophic lateral sclerosis. An absence of DSCR1L expression was observed in 7 of 8 libraries from subjects with Alzheimer's disease. A claimed method for detecting differential expression of a nucleic acid encoding DSCR1L alpha can be used to diagnose Down syndrome, Alzheimer's disease and other forms of dementia. A probe from such a nucleic acid is useful for identifying naturally occurring molecules encoding DSCR1L alpha, allelic variants or other molecules. The nucleic acids are useful for producing transgenic cell lines or organisms which model human disorders. They may also be used in gene therapy, and to screen for ligands which specifically bind the nucleic acid molecule, such as a DNA or RNA molecule, peptide nucleic acid, artificial chromosome, peptide, transcription factor, repressor or regulatory molecule, for use as a therapeutic.	XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation KW gene therapy; chromosome mapping; ss.
XX	SQ Sequence 3159 BP; 926 A; 657 C; 657 G; 915 T; 4 other; Query Match Score 211; DB 24; Length 3159; Best Local Similarity 65.2%; Pred. No. 5.6e-53; Matches 332; Conservative 0; Mismatches 165; Indels 12; Gaps 1;	XX DE 06-OCT-2000 (first entry)
QY 13 GATCTGAGCCTGGCGGCCAACCTGGCCACCTGGACCCGGCGGTGTTGCTG 72	XX DT 06-OCT-2000	
Db 371 GACTCATATGACCTCCCACACTGTTGGTGTGATAGCTGTGAA 430	XX XX	
QY 73 GAGGGCTGTGGGGCAAAATTGAACTCTTCAGAACATGAGAACACAC 132	XX XX	
Db 431 GAGAAAGAGCAAGGAAAATTGGAGGACINTTGGACTATGATGACTGTGAC 490	XX XX	
QY 133 TCCAGATTTAAAGCTCAACAGTGTCCGATAAACCTGAAACCCTTATCTGA 192	XX XX	
Db 491 TTCCAGTTTAAAGCTTACAGCTTACAGCTCTAACTCTAGCATCTAAATCTGA 550	XX XX	
QY 193 GCGGATGCCAGGCTGGGTGACAAGACGAGTTCCTGGGAAGGAAATGAAAGTTGAT 252	XX XX	
Db 551 GCGCAGGATAGCTTACAGCTTACGAAACCTAACATCAAGGAAAAAAATAAAGCTCA 610	XX XX	
QY 253 TTTCGCTAGACT-----TTACACATAGGAGTCAACCTGGCTCGCCAA 300	XX SQ Sequence 442 BP; 127 A; 111 C; 93 G; 111 T; 0 other;	
Db 611 TTGGCACAGGTTCAAGACTCAGAGACAGATGGAGACAATCTGACTCTGCTACCCCAAG 670	Query Match Score 207; DB 21; Length 442; Best Local Similarity 80.2%; Pred. No. 3.5e-52; Matches 24; Conservative 0; Mismatches 60; Indels 0; Gaps	
QY 301 CGCGACAAACAGTTCCTCATCCTCCCTCGGCCCTCTCCCTGGTAAACAGTA 360	QY 31 AGCCACCATCGCTGCCACCTGGACCGGGCTGTTGTTGAGGGCC 90	
Db 671 CCTGCCAACAGTTCTTCATCCTCCCTCGGCCCTCTCCCTGGTAAACAGTA 730	Db 140 AGCTCCCTGATGCTGTTGCAAACTAGTATCTCAGGAATGAAACAGGGCC 199	
QY 361 GAAGATGCCACCCCGCTCATATAATTAGCATCTTATATGCCATCTCAAGCTGGGCCA 420	QY 91 AAATTGAACTCCCTGATTCAGACATATGACAAGAACACCTTCAGTATTTAAGAGC 150	
Db 731 AACGATGCCACCGCACTGCTCAACTATGACCTCCCTCATGCTTGGCCAATAGACCA 790	Db 200 AAATTGAGTCCTCCCTGATGACCTGAACTCATCACCTTCAAGTATTAAGAGC 259	
QY 421 GGAGAGAACTGATGAACTGATCAGGCCACAGAACCCACTCCAGTGGTCCAGTG 480	QY 151 TTCAAACAGTGTCCGGATAAAACTCAGCAACCCPITATCTCAGGCCATCCAGGTGGCG 210	



PR	22-SEP-2000; 2000US-234509P.	Qy	87 GGCCAAATTGAAATCCTCTCAGAACATATGACAAGGACACCACCTTCCAGTTTAA 146
PR	22-SEP-2000; 2000US-234567P.	Db	276 GGAAAATTTGGGGACTGTTGGACTTGGACTTGGACTTGGACTTGGACTTGGACTTAA 335
PR	25-SEP-2000; 2000US-234933P.	Qy	147 GAGCTCAAACTGTCCGGATAACTTCAGAACCCCTTANCTGCAGGATGCCAGCT 206
PR	25-SEP-2000; 2000US-234942P.	Db	336 GAGTTTCAGACGTGTCGTATAAACCTCAGAAATCTGAGCCGAGCTGGAT 395
PR	25-SEP-2000; 2000US-235077P.	Qy	207 GCGGTCACAGAACGAGTTCTGGGAAGGAAATGAAAGTGTATTTGGCTCAGACT-- 264
PR	25-SEP-2000; 2000US-235149P.	Db	396 AGAGCTCATGAAACCAATCAGAGGAAAAAATAAAGCTCTACTTGCACAGGTPCA 455
PR	25-SEP-2000; 2000US-235209P.	Qy	265 -----TTACACATAGGAAGTTCACACTGGCTCCGGCAAATCCGACAACAGTT 314
PR	26-SEP-2000; 2000US-235637P.	Db	456 GACTCCAGAGAGAGATGGACAAACTGGCAGTGGCACCTGGCTCCACCCCAGCTGCCAAACAGTT 515
PR	26-SEP-2000; 2000US-235638P.	Qy	315 CCTCATATTCCCTCGGCTCTCGTGGCTGAAACAGTGAAGATGCCACCC 374
PR	28-SEP-2000; 2000US-236022P.	Db	516 TCTCATCTGGCCCCCTTCCTCCACCTGTGAGCTGGAGCCATAACAGATGCCCGCC 575
PR	28-SEP-2000; 2000US-236034P.	Qy	375 CGTCATTAATTAGCATTTTATATGCCATCTCCAACCTGGGCCACGGAGAAAGTGA 434
PR	28-SEP-2000; 2000US-236109P.	Db	576 AGTCCTAACATGACCTCCCTATGGTGTGCCAAACTAGGACCGAGAGATGTA 635
PR	28-SEP-2000; 2000US-236111P.	Qy	435 ACTGCTATGCGAGGAGACACCCACTCCAGTGTTGACGTGAGGTGACCA 494
PR	29-SEP-2000; 2000US-236833P.	Db	636 GCTCCATGCGAGGAGCTAGTCACCCAAAGTCTCGTCGTCGAGCTGAGTCAT 695
PR	28-SEP-2000; 2000US-236038P.	RESULT 15	
PR	28-SEP-2000; 2000US-236032P.	ID	ABL65187 standard; DNA; 3184 BP.
PR	02-OCT-2000; 2000US-236891P.	XX	
PR	02-OCT-2000; 2000US-237112P.	AC	ABL65187;
PR	02-OCT-2000; 2000US-237113P.	XX	15-MAY-2002 (first entry)
PR	02-OCT-2000; 2000US-237228P.	DE	Lung cancer related gene sequence SEQ ID NO:3524.
PR	02-OCT-2000; 2000US-237294P.	XX	XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; dangerous; cytostatic; gene therapy; anti neoplastic; Wilms' tumour; adenocarcinoma; gene; ds.
PR	02-OCT-2000; 2000US-237295P.	XX	XX Homo sapiens.
PR	02-OCT-2000; 2000US-237316P.	OS	W0200194629-A2.
PR	03-OCT-2000; 2000US-237435P.	XX	XX
PR	03-OCT-2000; 2000US-237598P.	DE	13-DEC-2001.
PR	03-OCT-2000; 2000US-237604P.	XX	XX
PR	03-OCT-2000; 2000US-237668P.	PR	05-JUN-2000; 2000US-209473P.
PR	03-OCT-2000; 2000US-237725P.	XX	XX
PR	01-NOV-2000; 2000US-244837P.	PR	05-JUN-2000; 2000US-209531P.
PR	01-NOV-2000; 2000US-245084P.	XX	PR 18-SEP-2000; 2000US-233133P.
XX	(AVAL-) AVALON PHARM.	XX	PR 18-SEP-2000; 2000US-233617P.
PA	PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;	PR 20-SEP-2000; 2000US-234009P.	
PA	PI Soppet DR, Weaver Z;	PR 20-SEP-2000; 2000US-234034P.	
PA	DR WPI: 2002-188264/24.	PR 20-SEP-2000; 2000US-234052P.	
XX	PT Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set -	PR 22-SEP-2000; 2000US-234509P.	
PT	PT	PR 22-SEP-2000; 2000US-234567P.	
PT	PR	PR 25-SEP-2000; 2000US-234923P.	
XX	PS Claim 1: SEQ ID 105; 44pp; English.	PR 25-SEP-2000; 2000US-234924P.	
XX	The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL6164 to ABL7010), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.	PR 25-SEP-2000; 2000US-235077P.	
XX	SQ Sequence 3184 BP; 921 A; 681 C; 657 G; 925 T; 0 other;	PR 25-SEP-2000; 2000US-235082P.	
XX	Query Match 32.3%; Score 193; DB 24; Length 3184;	PR 25-SEP-2000; 2000US-235134P.	
Best Local Similarity 67.4%; Pred. No. 1.5e-41;	Matches 293; Conservative 0; Mismatches 130; Indels 12; caps 1;	PR 25-SEP-2000; 2000US-235280P.	
PR 26-SEP-2000; 2000US-235637P;	PR 26-SEP-2000; 2000US-235638P.		

PR	27-SEP-2000; 2000US-235711P.	Db	396 AGAGCTTCAATGAAACCAAATTCAAGGGAAAAAAATTAAGCTTACTTTGCACAGGTCA 455
PR	27-SEP-2000; 2000US-235720P.	Qy	265 -----TTACACATAGGAAGPTCACACTGCTCCCCCATTCCCGACAAACAGTT 314
PR	27-SEP-2000; 2000US-235840P.	Db	456 GACTCCAGAGACAGATGAGACAANACTGCACTTGGCTTCACCCAGGCCCTGCAAAACAGTT 515
PR	27-SEP-2000; 2000US-235863P.	Qy	315 CCTCATCTCCCTCCGGCTCTCCCTCCGGCTCTGGTGAAGATGGCAACCC 374
PR	28-SEP-2000; 2000US-236028P.	Db	516 TCTCATCTGCCCTTCCTCCACACTGTAGCTGAGGCCATCAAGATGCCAGGCC 575
PR	28-SEP-2000; 2000US-236031P.	Qy	375 CGTCATAAATTACGATCCTTATATGCACTCTCCAAAGCTGGGCCAGGAGAACTATGTA 434
PR	28-SEP-2000; 2000US-236034P.	Db	576 AGTCCCTAACATGACCTCCCTATGACTCTGCAAAACTGGCCAAACTAGGACAGAGATGTA 635
PR	28-SEP-2000; 2000US-236109P.	Qy	435 ACTGATGCAAGGACAGACCCACTCCAGTGTCACCGTGTGAGACTGACCA 494
PR	28-SEP-2000; 2000US-236111P.	Db	636 GCTCCATGGAGGACTGAGTCACCCCAAGTGTCGTCAGCTGACAGTCAGT 695
PR	29-SEP-2000; 2000US-236842P.	Qy	495 AGAGAATGAGGAGGA 509
PR	29-SEP-2000; 2000US-236891P.	Db	696 AGAGGAGAAGAGGA 710
PR	02-OCT-2000; 2000US-237172P.		
PR	02-OCT-2000; 2000US-237173P.		
PR	02-OCT-2000; 2000US-237278P.		
PR	02-OCT-2000; 2000US-237294P.		
PR	02-OCT-2000; 2000US-237316P.		
PR	03-OCT-2000; 2000US-237425P.		
PR	03-OCT-2000; 2000US-23758P.		
PR	03-OCT-2000; 2000US-237604P.		
PR	03-OCT-2000; 2000US-237606P.		
PR	03-OCT-2000; 2000US-237608P.		
PR	01-NOV-2000; 2000US-244867P.		
PR	01-NOV-2000; 2000US-245084P.		
XX	(AVAL-) AVALON PHARM.		
XX	PA		
PI	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;		
PI	Soppet DR, Weaver Z;		
XX	WPI: 2002-188224/24.		
XX	PT		
PT	Screening for anti-neoplastic agent involves exposing cells to a		
PT	chemical agent to be tested for anti-neoplastic activity, and		
PT	determining a change in expression of a gene of a signature gene set -		
XX	PS		
XX	PA		
CC	The present invention describes a method (M1) for screening for an		
CC	anti-neoplastic agent. The method involves exposing cells to a chemical		
CC	agent to be tested for anti-neoplastic activity, determining a change in		
CC	expression of at least one gene (1) of a signature gene set, where (1)		
CC	comprises a sequence (S) selected from 8447 sequences (given in ABL61664		
CC	to ABL0110), or is at least 95% identical to (S), where a change in		
CC	expression is indicative of anti-neoplastic activity. (1) has cytosstatic		
CC	activity and can be used in gene therapy. M1 can be used for screening		
CC	an anti-neoplastic agent, and can be used for producing product which		
CC	is the data collected with respect to the anti-neoplastic agent as a		
CC	result of M1, and the data is sufficient to convey the chemical		
CC	structure and/or properties of the agent. M1 can be used in the		
CC	treatment of cancer such as colon, breast, lung, thyroid,		
CC	oesophageal, ovarian, kidney, prostate or pancreatic cancer,		
CC	adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,		
CC	infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine		
CC	carcinoma, papillary carcinoma and Wilms' tumour.		
XX	SQ Sequence 3184 BP: 921 A; 681 C; 657 G; 925 T; 0 other;		
Query Match	32.38;	Score	193; DB 24; Length 3184;
Best Local Similarity	67.4%	Pred.	No. 1.5e-47;
Matches	293;	Mismatches	0;
Conservative	0;	Indels	12;
		Gaps	1;
Qy	87 GCGCAATTTGATCCCTCGACATGACAGAGACCACTTCCAGTATTATAA 146		
Db	276 GGAAAAATTGGGGACTGTGGACTCTATGATGACTGTGAGCTGAGGTATTAA 335		
Qy	147 GAGCTTCAACTGTCGGATAACCTGAAACCCTTATCTGAGCCATGCCAGGT 206		
Db	336 GAGTTCAGACCTGTCGGTAAACTCGAACTTCTGAGCCGGAGCTTAGGT 395		
Qy	207 GCGGTGCAACGACCGAGTCCTGGGAAGAAATGAAAGTTCTCAGACT - 264		











APPLICANT : ROTHERMEL, BEVERLY  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE  
 FILE REFERENCE: UTSB-164P21  
 CURRENT APPLICATION NUMBER: US/09/782,953  
 CURRENT FILING DATE: 2001-02-13  
 PRIORITY APPLICATION NUMBER: 60/216,601  
 PRIOR FILING DATE: 2000-07-07  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 17  
 LENGTH: 3184  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (205)..(780)  
 S-09-782-953-17

	Query Match	Match Score	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Y	GGCCAATTGAAATCCTCTTCAGAACATPATGACAGGACACCCTTCCAGTTAA	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	276 GGAATAATTGGGGACTTGACTATGATGACTCTGGACTTCCAGCTATTAA	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	147 GAGCTCAAACGTGCGGATAAACTTCAGAACCCCTTATCTGCATGCCSATGCCAGGGCT 206	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	336 GAGTTCAAGGTGTCGTATAAACCTCAGAACCTTAATCTGCAGCCGGAGCTTAA	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	207 GCGGCTGCAAAAGACCGAGTCCCTGGGAAATGAAGTGTATTGCTCAGAT--	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	396 AGAGCTCAAGAACCCAAATTCAAGGGAAAATAAACCTCTACCTTCACAGTTCA	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	265 -----TTACACATAGGAAGGTACACCTGGTCCGCACAAACAGTT 314	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	456 GACTCGAGAGACATGGACAAACTGGACTTGGCTCCACCCAGCTGCCAAACAGTT 515	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	315 CCTCATCTCCCTCCGCCCTCCCTCCGCTTATATGCCATCTCCAGCTGGGCCGGAGAAGATGCA	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	516 TCTCATCTCGCCCCCTCCCTCCACCTGTTAGCTGGCAGCCCATAACGATGCCAGCC 575	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	375 CGTCATAAATTAGCACTTATATGCCATCTCCAGCTGGGCCGGAGAAGATGCA	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	576 AGTCCTCAACTATGACCTCTCTCTATGCTGTCGCAAAATTAGACCCGGAGAAGATGCA	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	435 ACTGTCGAGCAGCACCACTCCAGGTTGCACTGTGTGAGAGTGGACCA 494	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	636 GCTCCAGGAGCAAGTCCACCCAAAGTGTGCACTGTCGACAGTGCAGTACAT 695	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	495 AGAGATGAGGAGGA 509	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	
b	696 AGAGGAGAAGAGGA 710	32..38;	Score 193, DB 10;	67.4%	No. 2.7e-50;	0;	0;	

RESULT 11  
 JS-09-782-953-23  
 Sequence 23, Application US/09782953  
 ; Patent No. US2002010953A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ROTHERMEL, BEVERLY  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE  
 ; FILE REFERENCE: UTSB-164P21  
 ; CURRENT FILING DATE: 2001-02-13  
 ; PRIORITY APPLICATION NUMBER: 60/216,601  
 ; PRIOR FILING DATE: 2000-07-07  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 23

Query Match 31.2%; Score 186.4; DB 10; Length 828;  
 Best Local Similarity 61.8%; Pred. No. 1.4e-48;  
 Matches 320; Conservative 0; Mismatches 186; Indels 12; Gaps 1;

Qy 4 GAGGGTGGATCAGGACCTGGCACCCATGCCACTGGACCGCCGC 63  
 Db 134 GAGATGATTAAAGTGTCAGTCACTGAGTCCATGAAGCA 193

Qy 64 GTGTCGTGGACGGCCTGCGGGCCAAATTGATCCCTCTCAGACATAAG 123  
 Db 194 GTGTTGAGCACGAGGAAAGGATTTGAGACTCTACCATATGAC 253

Qy 124 GACACCACCTCCAGTATTAAAGACTGTCGGATAAACCTGAGAACCC 183  
 Db 254 CAGGTACTTTCAAGCTTAAAGCTTAAAGACTTAAATTAGAACCT 313

Qy 184 TTATCTGAGCCGATGCCAGGCTGGGTCAACAGCCAGGAAATG 243  
 Db 314 GAAGGGCACAAAGGCQAATAGAACCTCACGAAACAGACTAAC 373

Qy 244 AAGTGTATTTCGTCAG-----ACTTACACATAGGAGTCAACCTGGCT 291  
 Db 374 AAGCTATATTGACAGGGCAGATGTCGGAGAAGTGGGGACAAGTCCTC 433

Qy 292 CGGCCAATCCGACAAACGTTCTCATCCCTCCGGCTCTCCGGTGGCTG 351  
 Db 434 CGGCCCGCCAGCTGTCAGCGGTCTCATCCCTCCACCTCTCCAGTGGTGG 493

Qy 352 AAACAGTAGAAGATGCCACCCCGTCATAAATTAGATCTTATGCCATCTCCAAG 411  
 Db 494 AAGCAGAGCCAGATGGATGCCCTTATAATTAGTATTACTCTGTGTTCAAA 553

Qy 412 CTGGGCCAGAGATGGATGCCCTTATAATTAGTATTACTCTGTGTTC 471  
 Db 554 TTGGGACCAAGGAGAAATGAACTGAGCTGAGCCACCCAGGTGGTGC 613

Qy 472 GTCCACGTTGAGACTGAGAGTGGCAAGAGAATGAGGAGGA 509  
 Db 614 GTTCATGTCGTGAAAGTGAACCTGAGAGGAAGAGA 651

RESULT 13  
 US-09-782-953-8  
 ; Sequence 8, Application US/09782953  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILLIAMS, R. SANDERS  
 ; APPLICANT: ROTHERMEL, BEVERLY  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE  
 ; TITLE OF INVENTION: CALCIURIN INTERACTING PROTEIN (MCIP)  
 ; FILE REFERENCE: UTSID:674PZL  
 ; CURRENT APPLICATION NUMBER: US/09/782,953  
 ; CURRENT FILING DATE: 2001-02-13  
 ; PRIOR APPLICATION NUMBER: 60/216,601  
 ; PRIOR FILING DATE: 2000-07-07  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SEQ ID NO: 8  
 ; LENGTH: 594  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1) .. (591)

Query Match 30.7%; Score 183; DB 10; Length 594;  
 Best Local Similarity 61.7%; Pred. No. 1.4e-47;  
 Matches 341; Conservative 0; Mismatches 185; Indels 27; Gaps 2;

Qy 41 TCGCTGCCCCACTGGACCCGGCTGTCGGACGGCTGTGCCGAAATTGAA 100  
 Db 41 TCGCTGCTGGGGTCTTACCAATCAGGGTTTAAAGAAAAATTCGAGG 100  
 Qy 101 CCCTCTTCAGAACATATGACAAAGGACACCCATTCAGATTAAAGCTTCAAAGCTG 160  
 Db 101 GACTGTCGGACCTATGATTAATGTTGAGTTCAAGCTTAAAGAGTTTCGAGGG 160  
 Qy 161 TCGGATAAACCTCAGCAACCCCTATCTGAGGCCATGCCAGGCTGCGGTGACAGA 220  
 Db 161 TCGGATAAACATTACGCCATCCAAATCTGAGGCCATGCCAGGCTTCAAGT 220  
 Qy 221 CCGAGTCCCTGGAGAAATGAAAGTGTGTTTCCTCAG-----ACTTTAC 268  
 Db 221 CTCACTTCAGGGAGAAAGCTTAACACTCTACTCTCCCAGTCCAGACAG 280  
 Qy 269 ACATAGGAAGTTCACACCTGGCTCCGCCAATCCGCCAAACAGTCTCTCCCTC 328  
 Db 281 ATGGAAACAACTGCTATTGGACCCACGCCCTCAACAGTCTCTCACCC 340  
 Qy 329 CGGCCCTCTCCCTCCGGCTGGCTGGAAACAACTGAGATGGCCACCCCGTCAATAATTACG 388  
 Db 341 CTTCATCCTCCCTCTGTGGCTGGAAACCCCTATCAGCTGGCACAGTCTCAACTATG 400  
 Qy 389 ATCTTTTATGCTCCTCAGCTGGCAGGAGAACTGACTGACTGAGCTGAGCGA 448  
 Db 401 ACCCTCTTATGCTGGGCCAACCTGGACAGGAAATATGGCTGACGCTGGAA 460  
 Qy 449 CAGACCCCACTCCCACTGTTGGGTCACCGTGTGAGATGGCTGACCAAGAGATGAGGAGG 508  
 Db 461 CTGAGCTACACCGAGGGTCATGTGTGACAGGACATGGAGGAGGA-- 518  
 Qy 509 AAGGAAAGATGGAGAATGAGAACGACCCAAATCATCCAGACGGAGAC 568  
 Db 519 -----GGCCCAAGAGACTTCCCAAGGCCAAATCATCCAGACCCGCTC 565  
 RESULT 14  
 US-09-864-761-10388/C  
 ; Sequence 8, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Hank, David R.  
 ; APPLICANT: Hanel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEAR ACID PROBES USEFUL FOR  
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
 ; FILE REFERENCE: Acemic-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60,180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/332,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30

RESULT 15  
 US-09-864-761-2064/c  
 Sequence 2064, Application US/09864761  
 ; Patent No. US2002048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wenheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
 ; FILE REFERENCE: Acomics-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR APPLICATION NUMBER: US 60/236,359

---

Query Match 24.2%; Score 144.6%; DB 10; Length 412;  
 Best Local Similarity 89.1%; Pred. No. 1.2e-35; Indels 0; Gaps 0;  
 Matches 156; Conservative 0; Mismatches 19;

Qy	87	GCCAAATTGAACTCCCTCTAGAACATATGCAAGACACCACCTTCAGTTAA	146
Db	411	GGCAAATTGAGTCCCTTGTAGACCTATGAAAGACATACCTTTCAGTTAA	352
Qy	147	GAGCTTCAACGTTGCGGATAAACCTAGAACCCCTATCTGCGCCGATGCCGCT	206
Db	351	GAGCTTCAACGAGTCAGATAAACCTAGAACCCCTCTGGCAGATGCCGCT	292
Qy	207	GCGCTGCAAGAACGACTTCCGGGAAGGAAATGAGGTCTATTGCTCAG	261
Db	291	CCAGTGCAATAAGACTGAGTTCTGGAAAGGAAATGAGGTATATTGCTCAG	237

Query Match 24.2%; Score 144.6%; DB 10; Length 446;  
 Best Local Similarity 89.1%; Pred. No. 1.2e-35; Indels 0; Gaps 0;  
 Matches 156; Conservative 0; Mismatches 19;

Qy	87	GGCAAATTGAACTCCCTCTAGAACATATGCAAGACACCACCTTCAGTTAA	146
Db	445	GGCAAATTGAGTCCCTTGTAGACCTATGCAAGACATACCTTTCAGTTAA	386
Qy	147	GAGCTTCAACGTTGCGGATAAACCTAGAACCCCTATCTGCGCCGATGCCGCT	206
Db	385	GAGCTTCAACGAGTCAGATAAACCTAGAACCCCTCTGGCAGATGCCGCT	326

Query Match 24.2%; Score 144.6%; DB 10; Length 446;  
 Best Local Similarity 89.1%; Pred. No. 1.2e-35; Indels 0; Gaps 0;  
 Matches 156; Conservative 0; Mismatches 19;

Qy	207	GCGCTGCAAGAACGACTTCCGGGAAGGAAATGAGGTCTATTGCTCAG	261
Db	325	CCAGTGCAATAAGACTGAGTTCTGGAAAGGAAATGAGGTATATTGCTCAG	271

Search completed: November 15, 2002, 03:31:14  
 Job time : 57 secs

Gencore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2002, 01:34:13 ; Search time 1973 Seconds

(without alignments)  
4900.510 Million cell updates/sec

Title: US-09-575-580B-2

Perfect score: 597  
Sequence: 1 atggaggatggatctgca.....ccccatccacccatgtcgaa 597

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:

32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

```
1: em_estba:*
2: em_estthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mu:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*
```

RESULT 1

```
BQ749142 LOCUS BQ749142 520 bp mRNA linear EST 17-JUL-2002
```

```
DEFINITION UI-M-FDO-byd-c-04-0-UT.r1 NIH_BMAP_FDO Mus musculus cDNA clone  
IMAGE:7116339 5', mRNA sequence.
```

```
ACCESSION BQ749142 VERSION BQ749142.1 KEYWORDS EST.  
ORGANISM Mus musculus SOURCE house mouse.
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE 1 (bases 1 to 520) AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE Unpublished (1999) JOURNAL COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgraphs-r@mail.nih.gov
```

```
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Array by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGCG clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINN at:  
http://image.llnl.gov
```

```
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)
```

```
Seq primer: PYX-5.
```

```
Location/Qualifiers
```

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	518.4	86.8	520 14 BQ749142	BQ749142 UI-M-FDO-
2	507.8	85.1	1158 14 BQ955056	BQ955056 AGENCOURT
3	506.2	84.8	1507 11 AK010696	AK010696 Mus muscu
4	495.6	93.0	753 13 BT148584	BT148584 60291195
5	481.8	80.7	890 9 AL538796	AL538796 AL536447
6	481.4	80.6	828 9 AL536447	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.





BASE COUNT	ORIGIN	Query Match	Score	Length	DB	Site_1	NotI:
207	"Organ: liver; Vector: PCMV-SPORT; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP library."	83.0%;	Score 495.6;	Length 753;			
207	Best Local Similarity	99.0%;	Pred. No.	1-4e-121;			
207	Matches	509;	Conservative	0;	Mismatches	4;	Indels 1; Gaps 1;
Qy	84	CCGGCCCAATTGATCCCCCTTCAGAAATAATGACAAGGACACCCCTCCAGATT	143				
Db	171	CCAGGCCAATTGATCCCCCTTCAGAACATATGACAAGGACACCCCTCCAGATT	230				
Qy	144	TAAGACTTAAACGTGTCGGATAAACTCGAACCCCTTATCGCAGGCATGCCAG	203				
Db	231	TAAGACTTAAACGTGTCGGATAAACTCGAACCCCTTATCGCAGGCATGCCAG	290				
Qy	204	GCTGGGTGCGACAAGCGAGTCTCTGGGAGAAAATGAAGTTGATTTGCTCAGAC	263				
Db	291	GCTGGGTGCGACAAGCGAGTCTCTGGGAGAAAATGAAG-TGTATTTGCTCAGAC	349				
Qy	264	TTCACATGGAACTTCACCTGGCTCCGCCAATCCGACAAACAGTTCTCATCTC	323				
Db	350	TTCACATGGAACTTCACCTGGCTCCGCCAATCCGACAAACAGTTCTCATCTC	409				
Qy	324	CCCTCGGCCCTCTCCCTGGTGGAAACAACTGAGATGCCACCCTCATAAA	383				
Db	410	CCCTCGGCCCTCTCCCTGGTGGAAACAACTGAGATGCCACCCTCATAAA	469				
Qy	384	TTACGATCTTTATGCCATTCAGCTGGGCCAGGAGAAAGTGAACGTGCATGC	443				
Db	470	TTACGATCTTTATGCCATTCAGCTGGGCCAGGAGAAAGTGAACGTGCATGC	529				
Qy	444	AGCGACAGACCCACATCCACAGCTGGGGTCACTGTGTGAGGTGACAAAGAAATGA	503				
Db	530	AGCGACAGACCCACATCCACAGCTGGGGTCACTGTGTGAGGTGACAAAGAAATGA	589				
Qy	504	GGAGGAAGGAGAGATGGAGAAATGAGAGAACCCAGGCCAAATACTCCAGACAGC	563				
Db	590	GGAGGAAGGAGAGATGGAGAAATGAGAGAACCCAGGCCAAATACTCCAGACAGC	649				
Qy	564	GAGACCGGATCACACCGATCCACCTTAGCTGA	597				
Db	650	GAGACCGGATCACACCCATCCACCTCAGCTGA	683				
RESULT	5						
AL538796	LOCUS	AL538796	890 bp	mRNA	linear	EST 16-FEB-2005	
	DEFINITION	AL538796_LTI_FL013_FBrnl	Homo sapiens	cDNA clone	CS00DF037YL22	5	
	REFERENCE	1 (bases 1 to 890)					
	AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
	TITLE	Full-length cDNA libraries and normalization					
	JOURNAL	Unpublished (2001)					
	COMMENT	Contact: Genoscope					
		Genoscope - Centre National de Séquençage					
		BP 191 91006 EYRV cedex - France					
	FEATURES	Email: <a href="http://seqf@genoscope.cnrs.fr">seqf@genoscope.cnrs.fr</a> , Web : <a href="http://www.genoscope.cnrs.fr">www.genoscope.cnrs.fr</a>					
	source	Location/Qualifiers					
		1. .890					
		/organ="Homo sapiens"					
		/db_xref="taxon:9606"					
		/clone="CS00DF037YL22"					

```

/clone.lib="LTI_FL013_FBrnl"
/dev_stager="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
Maryland 20850, USA Fax : (1) 301 610 8371 Email :
http://fulllength.invitrogen.com"
http://fulllength.invitrogen.com"

BASE COUNT          207 a   246 c   280 g   157 t
ORIGIN

Query Match          80.7%; Score 481.8; DB 9; Length 890;
Best Local Similarity 89.1%; Pred. No. 7.4e-118;
Matches 532; Conservatve 0; Mismatches 62; Indels 3; Gaps 1;

Qy  1 ATGGAGGAGGTGGACCTTCAGGACCTGGCAGGCCACCATGCCCTGCCACCTTGACCGG 60
Db  205 ATGGAGGAGGTGGACCTTCAGGACCTGGCAGGCCACCATGCCCTGCCACCTTGACCG 264
Qy  61 CGCGTGTTCGTGGACCGGCCCTGTCGGCCGGCCAATTGGAATTCCTCTCAGAACATATGAC 120
Db  265 CGCGTGTTCGTGGACGGCCGTGTCGGCCGGCCAATTGGAATTCCTCTAAGGACTATGAC 324
Qy  121 AAGGACACCCATTCCAACTATTAAAGCTCTCAAACTGTCGGGATAAACCTGAGAAC 180
Db  325 AAGGACATCACCTTTCACTATTAAAGCTCTCAAACTGTCAGAACAACTTCAGAAC 384
Qy  181 CCCTTATGTGCAGCGATGCGAGGTGGCTGCACAGACCGAGATTCCTGGGAAGGA 240
Db  385 CCGCTTCGGACAGATGCCAGGCTCAAGCTGCTCATAGACTGAGTTCTGGRAAGGA 444
Qy  241 ATGAACTGTGTTATTTGCTCAAGACTTTACACATAGGAAGTTCACACCTGGCTCGGCCAAAT 300
Db  445 ATGAACTTATTTGCTCAAGCTTACACATAGGAACCTTCACACCTGGCTCGGCCAAAT 504
Qy  301 CCGGACACAGATGCTCATTCRCCCTCGGGCTCTCCCTGGAAACAACT 360
Db  505 CCAGACAACAGATTCGATTCRCCCTCGGGCTCTCCCTGGAAACAACTGGCTGGCCATCA 564
Qy  361 GAGATGCCACCCCCGTATAAATTAGCATCTTATAGCATCTTCACAGCTGGGCCA 420
Db  565 GAGATGGACCCCAGTATAACTATGATCTTATAGCCATCTCAAGCTGGGCCA 624
Qy  421 GGAGAGAGTGAACCTGATGGCAGGAAGGCCACTCCAGTGTGTTGCTCACGTC 480
Db  625 GGAGAAAATGATAATTGCAACGGAGCTGACACCACTCCAGCGTGTGGCCATCA 684
Qy  481 TGTGAGACTGACCAAGAGATGAGGAGAGAGAGAGATGAGAGATGAGAGACCC 540
Db  685 TGTGAGACTGATCAAGAGAGGAGAGAGAGAA---ATGAAAGATGAGAGACT 741
Qy  541 AACCCCAAAATCATCCAGACCGAGACGGAGTACACCGATCCACCTTAGCTGA 597
Db  742 AACCCCAAAATCATCCAGACCGAGACGGAGTACACCGATCCACGGATCCACCTCAGCTGA 798

RESULT 6
AL536447
LOCUS          AL536447 LTI_FL013_FBrnl 828 bp  mRNA  linear EST 13-FEB-2001
DEFINITION      AL536447 mRNA sequence.
PRIMER_AL536447
ACCESSION      AL536447.1 GI:12799940
KEYWORDS      EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```





Page 8

BASE COUNT	210 a	295 c	155 t	6 others
<b>ORIGIN</b>				
Query Match	78.5%	Score 468 ; DB 9;	Length 923;	
Best Local Similarity	88.4%	Pred. No. 2.5e-114;		
Matches	528;	Mismatches 3;	Indels 4;	Gaps 2
Y	1 ATGGAGGAGGTGATCTGCAGGACCTGCGCAGGCCACCATGCCTGCCACCTGGACCCG 60			
b	257 ATGGAGGAGGTGACCTGAGGCCCTGAGGACCTGCCAGGGCCACATCGCCCTGACCTGGACCCG 316			
Y	61 CGCGTGTCTGTTGAGCCGCTTGCGCCGCCAAATTGTGATCCCCCTTCAGAACATATGAC 120			
b	317 CGCGTGTCTGTTGAGCCGCTTGCGCCGCCAAATTGTGATCCCCCTTCAGAACATATGAC 376			
Y	121 AAGGACACCACCTTCAGCTATTATAAGGCTTCAAACGCTGTCGGGATAAACATTCAGCAC 180			
b	377 AAGGACATCACCTTTCAGTATTATAAGGCTTCAAACGACTCAAGAACATTCAGCAC 436			
Y	181 CCCATTATCTGCACGCCGATGCCAGCTGGGTGCAAGAACGGGTCTCTGGGAAGGAA 240			
b	437 CCCATTCTCGCAGCAGTGCCAGGCTCAGTGCTACATGCTGATTCAGTTCTGGGAAGGAA 496			
Y	241 ATGAAAGTGTATTTGGCTCAGACTTACATAGGAATGTCACCTGGCTCCCCCAT 300			
b	497 ATGAAAGTATATTTGGCTCAGACTTACATAGGAATGTCACCTGGCTACACCTGGCTCCCCCAT 556			
Y	301 CCCGACAAACAGTCTCCATCTCCCCTCCGGACTCTCTCCCGTTGGCTGGTAACAAGTA 360			
b	557 CCAGACAAAGCAGTCTCCATCTCCCCTCCGGCTCTCGCOATGGTGGTAACAAGTG 616			
Y	361 GAAAGTGCACCCCGCTGATAAATTAGATCTTTATATGCCATCTCAAGCTGGGCCA 420			
b	617 GAAAGTGCACCCCGCTGATAAATTAGATCTTTATATGCCATCTCAAGCTGGGCCA 676			
Y	421 GGAGAAAGTATGACTGCTATGCCAGAGACAGCCCAACTCCAGTGTGGTCCACGTG 480			
b	677 GGGAAAGATGAAATTGCACTGAGGACTGACCCCTCCAGCTGGGTCTCATGTA 736			
Y	481 TGTGAGAGTACCAAGAGATGAGGAAGGAAAGGAGAGGAGGAGGAGGAGGAGGCC 540			
b	737 TGTGAGAGTACCAAGAGGAGGAGGAGGAA --ATGGAAGAATGAGGAGA--CT 792			
Y	541 AAGCCAAAATCATCCAGACAGCAGGAGACGGGACTACACCCGATCCACCTTAGCTGA 597			
b	793 AAGCCAAAATCATCCAGACAGCAGGAGACGGGACTACACCCGATCCACCTTAGCTGA 849			
<b>RESULT 1.1</b>				
ORGANISM	BG915568	711 bp	mRNA	linear EST 05-JUN-20
DEFINITION	60215815F1 NC_1_CGAP_Mam4	Mus musculus	cDNA clone IMAGE:4945346 5	
mrNA sequence				
ACCESSION	BG915568			
VERSION	BG915568.1			
KEYWORD	EST			
SOURCE	mouse			
ORGANISM	Mus musculus			
MARYKOTE	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
MAMMALIA	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
REFERENCE	1 (bases 1 to 711)			
AUTHORS	NIH-NCG http://mgc.nci.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			

JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabps-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.
CDNA Library Preparation:	Life Technologies, Inc.
CDNA Library Arrayed by:	The T.M.A.G.E. Consortium (LNL)
DNA Sequencing by:	Incyte Genomics, Inc.
Clone distribution:	MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Plate:	LIM010891 row: n column: 03
High quality sequence stop:	711.
Location/Qualifiers	1..711
/organism="Mus musculus"	
/strain="NMRI"	
/db_xref="taxon:10090"	
/clone_lib="NCI_CGAP_Man4"	
/tissue_type="tumor, gross tissue"	
/dev_stage="5 months"	
/lab_host="DH1.0B"	
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal Site_2: NotI; Cloned unidirectionally; Primer: Oligo d Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Group and Differentiation 7, 3-11 (1996)."	
FEATURES	
Source	
BASE COUNT	
ORIGIN	
Query Match	Score 465.4; DB 13; Length 711;
Best Local Similarity	98.0%
Matches 491; Conservative 0; Mismatches 6; Indels 2; Gaps	Pred. No. 1..6-113; Site_1: Sal
Qy 84 CCGGGCCAAATTGTGAATCCCTCTTCAGAACATATGCCAAGGCCACCCATTCCAGTATT	Site_2: NotI
Db 62 CCAGGGCCAAATTGTGAATCCCTCTTCAGAACATATGCCAAGGCCACCCATTCCAGTATT	Cloned unidirectionally
Qy 144 TAAGAGCTTCAAAACGTTCCGGATAAAACTTCAAGAACCCCTTATCTGCCAGCGATGCCAG	Primer: Oligo d
Db 122 TAAGAGCTTCAAAACGTTCCGGATAAAACTTCAAGAACCCCTTATCTGCCAGCGATGCCAG	Library constructed by Life Technologies. Investigators
Qy 204 GCTGGGGCTGCAAAAGCCGACTTCCTGGGAGGAAATGAAGTTGTTATTGTCAGAC	providing samples: Lothar Hennighausen/Priscilla Furth,
Db 182 GCTGGGGCTGCAAAAGCCGACTTCCTGGGAGGAAATGAAGTTGTCAGAC	NIH Reference for transgenic model: Li et al., Cell Group
Qy 264 TTTCACATAGGAAAGTCACACTGGCTTCACACTGGCTTCACACTGGCTTCAC	and Differentiation 7, 3-11 (1996)."
Db 242 TTTCACATAGGAAAGTCACACTGGCTTCACACTGGCTTCACACTGGCTTCAC	
Qy 324 CCCTCGGGCCCTT-CCTCCGGTGGTGGAAACAACTGAAAGATGCCACCCCGTCAAA	
Db 302 CCCTCGGGCCCTTCCCTCCGTTGGTGGAAACAACTGAAAGATGCCACCCCGTCAAA	
Qy 383 ATTACGATCTTATATGCCATCTCAAGCTGGGGCAGGAGAAGTATGAACTGGCATG	
Db 362 ATTACGATCTTATATGCCATCTCAAGCTGGGGCAGGAGAAGTATGAACTGGCATG	
Qy 443 CACGGACAGACCCCACTCCAGTGTTGCTACGTGTTGAGATGCCAGAACAAATCATCCAGAC	
Db 422 CACGGACAGACCCCACTCCAGTGTTGCTACGTGTTGAGATGCCAGAACAAATCATCCAGAC	
Qy 503 AGGAGAAAGGAGAGATGGAGAAATGAAGAACCCAAAGGCCAAATCATCCAGAC	
Db 482 AGGAGAAAGGAGAGATGGAGAAATGAAGAACCCAAAGGCCAAATCATCCAGAC	
Qy 563 GGAGCAAGGGAGTACNACC	
Db 541 GGAGCAAGGGAGTACNACC	

RESULT	12	Qy	483	TGAGAGTGCACCAAGAATGAGGGAAACAGGAA-GAGATGGAGAATG-AAGAGACCC	540
LOCUS	BF782633	Db	557	TGAGAGTGCACCAAGAATGAGGGAAACAGGAA-GAGATGGAGAATG-AAGAGACCC	616
DEFINITION	602107462F1 NCI_CGAP_Kid14 Mus musculus CDNA clone IMAGE:4236038				
5' mRNA sequence.					
ACCESSION	BF782633	Qy	541	AAGGCCAAATCATCAGCACCGGACTAACACCGATCACCTTAGCTGA	597
VERSION	BF782633.1	Db	617	AAGGCCAAATCATCAGCACCGGACTAACACCGATCACCTAGCTGA	673
KEYWORDS	house mouse.				
ORGANISM	Mus musculus				
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus .					
REFERENCE	1 (bases 1 to 950)	RESULT	13	TGAGAGTGCACCAAGAATGAGGGAAACAGGAA-GAGATGGAGAATG-AAGAGACCC	540
AUTHORS	NH-MGC http://mgc.ncbi.nlm.nih.gov/	LOCUS	BG296537	980 bp mRNA linear EST 21-FEB-2001	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	DEFINITION	602394141F1 NIH_MGC_94	Mus musculus cDNA clone IMAGE:4506130 5' , mRNA sequence.	
JOURNAL	Unpublished (1999)	ACCESSION	BG296537		
COMMENT	Contact: Robert.Strausberg@nih.gov	VERSION	BG296537.1	EST.	
	Email: cgabbs@nlm.nih.gov	KEYWORDS			
	Tissue Procurement: Jeffrey E. Green, M.D.	SOURCE			
	CDNA Library Preparation: Life Technologies, Inc.	ORGANISM			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)	Mus musculus			
	DNA Sequencing by: Incyte Genomics, Inc.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus .			
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at:	REFERENCE	1 (bases 1 to 980)	NH-MGC http://mgc.ncbi.nlm.nih.gov/.	
	Plate: LLM9843 row: k column: 15	AUTHORS		National Institutes of Health, Mammalian Gene Collection (MGC)	
	High quality sequence stop: 701.	TITLE		Unpublished (1999)	
FEATURES	Location/Qualifiers	JOURNAL		Contact: Robert.Strausberg@nih.gov	
source	1..950	COMMENT		Email: cgabbs@nlm.nih.gov	
	/organism="Mus musculus"			Tissue Procurement: The Cepko Laboratory	
	/strain="FVB/N"			CDNA Library Preparation: Life Technologies, Inc.	
	/db_xref="txxon:10090"			CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)	
	/clone="IMAGE:4236038"			DNA Sequencing by: Incyte Genomics, Inc.	
	/clone.lib="NCI_CGAP_Kid14"			Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at:	
	/lab_host="DH10B (TM) phage resistant"			http://image.llnl.gov	
	/note="Organ: Kidney; Vector: pcMV-SPORT6; Site:1: NotI;	Plate:	LLAM10381	row: a column: 11	
	Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.			High quality sequence start: 3	
	Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library.  "			High quality sequence stop: 747.	
BASE COUNT	220 a 257 c 274 g 199 t	FEATURES		Location/Qualifiers	
ORIGIN		source		1..980	
				/organism="Mus musculus"	
				/db_xref="taxon:10090"	
				/clone="IMAGE:4506130"	
				/clone.lib="NH_MGC_94"	
				/tissue_type="retina"	
				/lab_host="DH10B (phage-resistant)"	
				/note="Organ: eye; Vector: pcMV-SPORT6; Site:1: NotI;	
				Site:2: SalI; Cloned unidirectionally; oligo-dT primed.	
				Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.	
				Note: this is a NH_MGC Library."	
				BASE COUNT	265 a 258 c 269 g 188 t
				ORIGIN	
Query Match	77.3%			Score 463.4; DB 12; Length 950;	
Best Local Similarity	96.3%	Pred.	No. 6.2e-113;		
Matches 517; Conservative	0;	Mismatches	16;	Best Local Similarity 96.2%; Pred. No. 2.2e-112;	
		Indels	4;	Mismatches 0; Mismatches 16;	
		Gaps	4;	Indels 4; Gaps 3;	
Qy	64	Db	138	GTCCTTCGGTGGACGCCAAATTGAAATCCTCTTCAGAACATATGACAAAG 123	123
				GTCCTTCAGGAAAGTGAAACCGGGCCAATTTGAAATCCTCTTCAGAACATATGACAAAG 197	207
Qy	124	Db	198	GACACCACCTTCAGTATTAGAGCTTCAAACGTGTCGGATAAACTTCAGCAACCC 183	183
				GACACCACCTTCAGTATTAGAGCTTCAAACGTGTCGGATAAACTTCAGCAACCC 257	267
Qy	184	Db	258	TATCTGAGCCATGCGGCTTCGGTGGAGGAATG 243	243
				TATCTGAGCCATGCGGCTTCGGTGGAGGAATG 303	303
Qy	244	Db	318	AAGTTGTTATTCGAGCTTACACATAGGAAATTCACACTGGCTCGGCCAATCC 436	436
				GATGCCACCCCGCATAAATTAGATCTTATGCACTTCGGCCATCGGCTCGGCCAAGA 317	376
Qy	364	Db	377	GATGCCACCCCGCATAAATTAGATCTTATGCACTTCGGCCATCGGCTCGGCCAAGA 363	363
				GATGCCACCCCGCATAAATTAGATCTTATGCACTTCGGCCATCGGCTCGGCCAAGA 496	496
Qy	424	Db	437	GAGAAGTATGAACTGCACTGGACACACCCACTCCAGT GTGGTGTCCACGTG 482	482
				GATGCCACCCCGCATAAATTAGATCTTATGCACTTCGGCCATCGGCTCGGCCAATCC 556	556
Qy	424	Db	497	GAGAAGTATGAACTGCACTGGACACACCCACTCCAGT GTGGTGTCCACGTG 386	386

QY	304	GACAAACAGTCCCATCCTCCCCCTCGGCCCTCCGTGGAAACAAGTAGAA	363	Db	219	TAAGACCTTCATAACGTTGGGATAAACCTICAGCAACCCCTATCTGGAGCCATGCCAG	278
Db	387	GACAAACAGTCCCATCCTCCCCCTCGGCCCTCCGTGGAAACAAGTAGAA	446	QY	204	GCTGGCGCTGCACAGACGCGAGTCTGGGAAGAAAGTGTATTGCTCAGAC	263
QY	364	GATGCCACCCCGTCATAAATTAGATCCTTATGCTCCAGTGGCCAGGA	423	Db	279	GCTGCCTGCGACAAAGCCAGTTCCTGGGAAGAAAGTGTATTGCTCAGAC	338
Db	447	GATGCCACCCCGTCATAAATTAGATCCTTATGCTCCAGTGGCCAGGA	506	QY	264	TTTACACATAGAAGTTCACACTGGTCGGCCAAATCCGACAAACAGTTCCTCATCTC	323
QY	424	GAGAACTGAACTGCTGGGACAGACCCACTCCAGTGTCGTCAGTGT	483	Db	339	TTTACACATAGAAGTTCACACTGGTCGGCCAAATCCGACAAACAGTTCCTCATCTC	398
Db	507	GAGAACTGAACTGCTGGGACAGACCCACTCCAGTGTCGTCAGTGT	566	QY	324	CCCTCGGCCCTCTCCCTGGGTGGTGAACAAGTAGANGATGCCACCCGTCATAAA	383
QY	484	GAGATGACCAAGAGAATGGGAGAGAATGAGAGACCCAAAG	543	Db	399	CCCTCGGCCCTCTCCCTGGGTGGTGAACAAGTAGANGATGCCACCCGTCATAAA	458
Db	567	GAGATGACCAAGAGAATGGGAGAGAATGAGAGACCCAAAG	624	QY	384	TTCAGTACCTTTATATGCCCTCCCTGGGTGGTCACTGGTGGAGACTGACATGC	443
QY	544	CCCAAATCATCCAGACGGGAGCACCCATCCAGTGTCGTCAGTGT	588	Db	459	TTCAGTACCTTTATATGCCCTCCCTGGGTGGTGGAGAGTGAACATGCATGC	518
Db	625	CCCAAATCATCCAGACGGGAGCACCCATCCAGTGTCGTCAGTGT	668	QY	444	ACGGACAGACCCACCTCCAGTGTGGTGGTCACTGGTGGAGACTGACATGC	503
RESULT	14			QY	519	ACGGACAGACCCACCTCCAGTGTGGTGGTCACTGGTGGAGACTGACATGC	578
LOCUS	B1219142	665 bp	mRNA	QY	504	GGAGGAAGGAGAGATGGAGAATGAAG-ACCAAGCCAAATCATCCAGACA-	561
DEFINITION	602935788F1	NCL_CGAP_L19	Mus musculus	Db	562	CGGAGACGGAGTACACCGATCCA	587
ACCESSION	B1219142		CDNA clone IMAGE:5099372	QY	579	GGGAGACGGAGTACACCGATCCA	664
VERSION	B1219142.1			Db	639	CGGAGACGGAGTACACCGATCCA	
KEYWORDS				RESULT	15		
SOURCE	ORGANISM	Mus musculus		LOCUS	BB617325	BB617325	BB617325
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		DEFINITION	BB617325	710 bp	mRNA
		Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.		REFERENCE	BB617325	lineар	linear
		1 (bases 1 to 710)		AUTHORS	BB617325	EST	EST
REFERENCE	1 (bases 1 to 665)			DEFINITION	BB617325	enriched	26-OCT-2001
AUTHORS				ACCESION	BB617325	11 days pregnant female	
TITLE	NIH-MCG	http://mgc.ncbi.nih.gov/		VERSION	BB617325.1	ovary and uterus	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			KEYWORDS	GI:16457186	Mus musculus	
COMMENT	Unpublished (1999)			ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Contact: Robert Strausberg, Ph.D.			DEFINITION		Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.	
	Email: cgaps-remail.nih.gov			REFERENCE		1 (bases 1 to 710)	
	Tissue Procurement: Jeffrey E. Green, M.D.			AUTHORS		Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.	
	CDNA Library Preparation: Life Technologies, Inc.			DEFINITION		Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koda	
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			VERSION		Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,	
	DNA Sequencing by: Incyte Genomics, Inc.			KEYWORDS		Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sano,H., Sasaki	
	Clone distribution: MCG clone distribution information can be			SOURCE		,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,	
	found through the I.M.A.G.E. Consortium/LLNL at:			ORGANISM		Tanami,M., Tagawa,A., Takashashi,F., Takeda,Y., Tanaka,T., Toya,T.,	
	http://image.llnl.gov/			DEFINITION		Muramatsu,M. and Hayashizaki,Y.	
	Plate: LLAM11238	row: o	column: 21	REFERENCE		RIKEN Mouse ESTS (Arakawa,T., et al. 2001)	
	High quality sequence stop: 657.			AUTHORS		Unpublished (2001)	
FEATURES	Source			DEFINITION		Contact: Yoshihide Hayashizaki	
	/organism="Mus musculus"			VERSION		Laboratory for Genome Exploration Research Group, RIKEN Genomic	
	/strain="FVB/N"			KEYWORDS		Sciences Center (GSC), Yokohama Institute	
	/db_xref="taxon:10090"			COMMENT		The Institute of Physical and Chemical Research (RIKEN)	
	/clone="IMAGE:5099372"			ORGANISM		1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan	
	/clone_lib="NCL_CGAP_L19"			DEFINITION		Phone: 81-45-503-9226	
	/lab_host="DH10B (T1 phage-resistant)"			REFERENCE		Fax: 81-45-503-9226	
	/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;			VERSION		Email: genome.rese@sc.riken.go.jp/	
	Site_2: Sall; Cloned unidirectionally; Primer: Oligo dT.			KEYWORDS		URL: http://genome.gsc.riken.go.jp/	
	Average insert size: 1.9 kb. Constructed by Life			COMMENT		Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh	
	Technologies. Note: this is a NCI_CGAP Library."			ORGANISM		,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	
BASE COUNT	192 a	170 c	158 g	DEFINITION		Normalization and subtraction of cap-trapper-selected cDNAs to	
ORIGIN	77	score 461.2;	DB 13;	COMMENT		prepare full-length cDNA libraries for rapid discovery of new	
Query Match	77.3%	Length 665;	Pred. No. 2.1e-112;	ORGANISM		genes. Genome Res. 10 (10), 1617-1630 (2000)	
Best Local Similarity	97.0%		Mismatches 0;	DEFINITION		wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,	
Matches 491; Conservative			Indels 2;	REFERENCE		Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsui	
QY	84	CGGGCCAATTGTAATCCCTCTGACAATATGACAGGACACCCATTCCAGATT	143	VERSION		,S., Kawai,J., Okazaki,Y., Morimatsu,M., Inoue,Y., Kira,A. and	
Db	159	CCAGGCCAAATTGTAATCCCTCTGACAATATGACAGGACACCCATTCCAGATT	218	KEYWORDS		Hayashizaki,Y.	
QY	144	TAAGAGCTCAAAACGTTGGGATAAAACTTCAGCAACCCCTTATCTGCAACCGATGCCAG	203	COMMENT		RIKEN integrated sequence analysis (RISA) system--384-format	

sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Kondo, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, K., Itoh, M., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

## FEATURES

## source

GAGAGAGAGGGATCCAGAGCTCTTTTTTTTTTNTVN 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCTCGGAAATTAAATTAACTCCCCCCCCC 3']. cDNA was cloned into the XbaI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

BASE COUNT    197 a    184 c    171 g    156 t    2 others  
ORIGIN

Query Match    75.9%    Score 453; DB 10; Length 710;  
Best Local Similarity    91.9%; Pred. No. 3.3e-110;

Matches 477; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 31 AGGCCACCATCGCTGGCCACCTGGACCCGGCGGTTCGGACGGCTTGCGGGC 90

Db 127 AGCTCCCTGATGCTGTGTGGCAAACGATGATGTCCTCACGGAAAGTGAGCAGGGCC 186

Qy 91 AAATTGAATCCCTCTCAAGACATATGACAGAACACCTTCCAGTATTAGAGC 150

Db 187 AAATTGAATCCCTCTCAAGACATATGACAGAACACCTTCCAGTATTAGAGC 246

Qy 151 TICAAACGTGTCGGATAAACCTCAGAACCCCTTATCTGGACGCCATGCCAGGTGCGG 210

Db 247 TICAAACGTGTCGGATAAACCTCAGAACCCCTTATCTGGACGCCATGCCAGGTGCGG 306

Qy 211 CTGCCACAAGCCGAGTTCTGGGAAGGAATGAAGTGTATTTCCTCAGCTTACAC 270

Db 307 CTGCCACAAGCCGAGTTCTGGGAAGGAATGAAGTGTATTTCCTCAGCTTACAC 366

Qy 271 ATAGGAAGTCAACCTGGTCGGCCAAATCCGAAACAGTCCCTCATGCCAGGTGCGG 330

Db 367 ATAGGAAGTCAACCTGGTCGGCCAAATCCGAAACAGTCCCTCATGCCAGGTGCGG 426

Qy 331 GCCTCTCCTCCGTTGGCTGGAAACAGTAGAGATGCCACCCCGTCATAAATTACGAT 390

Db 427 GCCTCTCCTCCGTTGGCTGGAAACAGTAGAGATGCCACCCCGTCATAAATTACGAT 486

Qy 391 CTTTTATGCCATCCTCAAGCTGGCCAGAGAAGATGACTGCAGGACA 450

Db 487 CTTTTATGCCATCCTCAAGCTGGCCAGAGAAGATGACTGCAGGACA 546

Qy 451 GACCCACTCCAGTGGTGGTCAAGGTGAGTGAAGTGAAGAATGGAGAA 510

Db 547 GACACACTCCAGTGGGNGTCCACGTGTTGAGGTGACCAAGAAATGGAGGAA 606

Qy 511 GAGGAAGATGGAGAAATGAGAGACGCCAAAGCCAA 549

Db 607 GAGGAAGAATGGAGAAATGAGAAATGAGAAANACCCAGCCAAA 645

Search completed: November 15, 2002, 03:28:51  
Job time : 1980 secs

THIS PAGE BLANK (uspto)